## STIC-Biotech/ChemLib

180630

From:

Salmon, Katherine D.

Sent:

Monday, February 27, 2006 9:03 AM

To: Subject: STIC-Biotech/ChemLib SEquence Request

HI, this is a sequence search request for case 10/720424.

- Please Search Seq ID No. 1
   please search seq id NO. 8
- 3. Please search SEQ ID NO. 1 with word hits under 100
- 4. Please search SEQ ID No. 8 with word hits under 100

Thanks Katherine Salmon ART UNIT 1634 Mailbox REM2C70

E3 27 20

\*\*\*\*\*\*\*\*
Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#\_\_\_\_\_ AA#:\_\_\_\_

S/L:\_\_\_\_ Oligomer:\_\_\_\_

Encode/Transl:\_\_\_\_

Structure #:\_\_\_\_Text:\_\_\_

Inventor:\_\_\_\_ Litigation:\_\_\_

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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Synthetic D

Macaca mu

Scoring\_table:

Word size

Database

Searched:

Perfect score:

ritle:

Run on:

Sequence:

monoclo

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DNA linear PAT 27-AUG-2002 human papilloma virus.
                  AR012649 Sequence
AR025701 Sequence
AR025701 Sequence
AK65947 Sequence
AK514339 Sequence
AK519906 Sequence
AX519906 Sequence
AX230265 Sequence
AX161516 Sequence
AX161516 Sequence
AX158711 Sequence
AX158713 Sequence
AX165871 Sequence
AX161519 Sequence
AX161519 Sequence
AX161513 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 38)

Bouna, S.K., Joseph, J.L., Marshall, R.L. and Laffler, T.G.

Nuclectide sequences useful as type specific probes, PCR primers and LCR probes for the amplification and detection of human papilloma virus, and related kits and methods

Patent: US 5484699-A 316-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14; DB 6; Length 38;
Pred. No. 1.8e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                         38 bp
Sequence 53 from patent US 5484699.
117042
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/organism="unknown"
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Short-chain nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                AR096779
CQ799486
CQ799486
AR665947
AR665947
AR665947
AR519309
AR519406
AR7230265
AR7230265
AR728744
AR161516
AR728748
AR16151
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100.0%; Pre
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JP 2001231587-A/53.
unidentified
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Best Local Similarity 100.
Matches 14; Conservative
GATGGTGATATGGT
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RESULT 1
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AX579956 Sequence
AX580273 Sequence
A71350 Sequence
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BD181525 Sequence
AX474340 Sequence
CQ809558 Sequence
CQ809558 Sequence
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BD017550 Short-cha
AY044145 Synthetic
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AX579734 Sequence
CQ808544 Sequence
CS125179 Sequence
AX378402 Sequence
                                                                            5, 2006, 22:12:24 ; Search time 1167.5 Seconds (without alignments) 1411.957 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                              5883141 segs, 28421725653 residues
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AX580273
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BD181525
AR575320
AR575320
CQ809558
NEUMTTRMF
                                                       OM nucleic - nucleic search, using sw model
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29
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8 8 8 8 8 8
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PAT 03-APR-1996

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AX579956.1 GI:27649158
                                                            AX578544.1 GI:27647746
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                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.

(bases 1 to 87)

Peng, R., Yao, Q., Xiong, A., Li, X. and Fan, H.

Direct Submission
Submitted (06-JUL-2001) Shanghai Yong Ye Agro-Bioengineering Co.,

Ltd, Shanghai Academy of Agricultural Sciences, Beidi Road 2901,
Shanghai 201106, China

Location/Qualifiers
                                                                                                                                                                                               C12N15/00,C12R1:93)
(C12N15/00,C12R1:93)
Strandedness: Single;
Topology: Linear;
Topology: Linear;
Location/Qualifiers
Location/Qualifiers
1. .38
                                                                                                                                                                                      RAHLER
CI2N15/09, CI2M1/00, C12Q1/68//(C12N15/09,C12R1:93),C12N15/00,
                                                                                                                                                                        JEFFREY L JOSEPH, STANLEY R BORMA, RONALD L MARSHALL, THOMAS G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .87
/organ="synthetic construct"
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/mol type="genomic DNA"
/db_xref="taxon:32630"
/nofe="contains five copies of the nitrogen regulatory element (ANACTA); can be inserted into lacZ reporter plasmid for yeast one-hybrid system"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Synthetic construct nitrogen regulatory cis element sequence.
AY044145
             Joseph, J.L., Borma, S.R., Marshall, R.L. and Rahler, T.G. Short-chain nucleotide sequence of human papilloma virus Patent: JP 2001231587-A 53 28-AUG-2001; ABBOTT LABORATORIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                          48.3%; Score 14; DB 6; Length 38; 100.0%; Pred. No. 1.8e+03; ive 0; Mismatches 0; Indels
                                                                           Unidentified
JP 2001231587-A/53
28-AMG-2001
31-JAN-2001
JP 2001023849
28-SEP-1990 US 589948, 28-SEP-1990 US
                                                                                                                                                                                                                                                                                                                                                  1. .38
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synthetic construct
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Best Local Similarity 100.
Matches 14; Conservative
                                                                           OS Unidentifie
PN 28-AUG-2001
PF 31-JAN-2001
PR 28-SEP-1990 US
PI JEFFREY L J
PI RAHLER
PC (CI2N15/00,
PC (CI2N15/00,
CC Strandednes
CC Strandednes
CC Short-chair
KRSY
FT SOURCE
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AY044145/c
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PAT 10-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 10-JAN-2003
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Method and reagent for the inhibition of calcium activated chloride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                   Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.
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Patent: WO 0211674-A 1794 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
                                                                                                                                                                                                                                                                                                                                                                                                                            (as)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                  channel-1 (clca-1)
Patent: WO 0211674-A 382 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC
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44.8%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels
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44.8%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels
  linear
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     RNA
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Sequence 1794 from Patent W00211674.
AX579956
AX578544 17 bp F
Sequence 382 from Patent WO0211674.
AX578544
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/organism="Homo gapiens"
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Location/Qualifiers
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Location/Qualifiers
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RESULT 6 AX580273

RESULT 4

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Gaps

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JOURNAL

TITLE

FEATURES

ORIGIN

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PAT 15-MAY-2003
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                                                                     Sahin,U., Tuereci,O. and Koslowski,M.
Genetic products differentially expressed in tumors and the use
thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1 (HIV-1)
Human immunodeficiency virus 1
Viruses, Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
                                                                                                                                                                               1. .21
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Oligonukleotid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1
JP 2002330790-A/1
19-NOV-2002
09-JAN-2002 JP 2002002066
09-JAN-2001 US 09/757207
TOBIN J HELLYER, QIMIN VOU, JAMES M HARRIS
Cl2N15/09,Cl2Q1/68,Cl2N15/00
Sequences and methods for detection of HIV-1
Key

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100.0%; Pred. No. 7.3e+03;
ative 0; Mismatches 0;
                                                                                                                     Parent: WO 2004047863-A 67 10-JUN-2004;
Ganymed Pharmaceuticals AG (DE)
Location/Qualifiers
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Hellyer, T.J., You, Q. and Harris, J.M.
Sequences and methods for detection of
Parent: JP 2002330790-A 1 19-NOV-2002;
BECTON DICKINSON AND CO
   synthetic construct
synthetic construct
other sequences, artificial sequences.
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JP 2002330790-A/1.
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                             Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
Patent: WO 0211674-A 2111 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
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   PAT 10-JAN-2003
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                                                                                      Homo sapiens (human)
Memo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                            Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.
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     linear
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Sequence 67 from Patent WO2004047863.
CQ821559
CQ821559.1 GI:49019333
   17 bp R1
Sequence 2111 from Patent W00211674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                44.8%; Score 13; DB 100.0%; Pred. No. 7.4; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="unassigned DNA"
/db_xref="taxon:32644"
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/organism="unidentified"
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Sequence 1 from Patent WO9811253.
A71350.
A71350.1 GI:4774983
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Location/Qualifiers
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unidentified
unclassified sequences.
1 (bases 1 to 21)
                                                      AX580273.1 GI:27649475
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Best Local Similarity 100.
Matches 13; Conservative
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mitochondrial tRNA.

Contributed on tape April 1983 by M.Sprinzl & D.H.Gauss; from their contributed on tape April 1983 by M.Sprinzl & D.H.Gauss; from their entry 1360 in Nucleic Acids Res. 11, r1-r54 (1983). N.crassa mt Met-tRNA-f resembles that of eukaryotic organisms in its structure, but its sequence honology is closer to prokaryotic sequences (although it resembles neither to any great extent [1]).

Location/Qualifiers
                   Lackso,I.J.
Genes and uses thereof to modulate secondary metabolite
Genes and uses thereof to modulate secondary wetabolite
biosynthesis w 2003097790-A 861 27-NOV-2003;
Vlaams Internniversitair Instituut voor Biotechnologie vz w. (BE);
VT Biotechnology (FI)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLN 20-MAY-1994
Inz, D.G., Goossens, A., Oksman-Caldentey, K.M., Haekkinen, S.T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurospora crassa

Neurospora crassa

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

1 (Dases I to 74)

Heckman, J.E., Hecker, L.I., Schwartzbach, S.D., Barnett, W.E.,

Brumetark, B. and RajBhandary, U.L.

Structure and function of initiator methionine tRNA from the

mitochondria of Neurospora crassa

(211 13 (1), 83-95 (1978)
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Original source_text: Neurospora crassa (strain or23-ia)
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N.crassa mitochondrial initiator Met-tRNA-f.
K00315
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44.8%; Score 13; DB 15; I
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                         Ouery Match
44.8%; Score 13; DB 6; Lv
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 13; Conservative 0; Mismatches 0;
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/organism="Neurospora crassa"
/organelle="mitochondrion"
/mol_type="tRNA"
/db_xref="taxon:5141"
1. .74
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/mod_base=OTHER

    .42
/organism="Nicotiana tabacum"
/mol_type="unassigned DNA"
/db_xref="taxon:4097"

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5' end of mature tRNA
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         PAT 14-DEC-2004
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Wkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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Human immunodeficiency virus 1
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
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0, 7.16+03; Indels
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/organism="Human immunodeficiency virus 1"
/mol_type="unassigned DNA"
/db_xref="taxon:11676"
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       linear
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Hellyer,T.J., You,Q. and Harris,J.M.
Sequences for detection of HIV-1
Patent: US 6770752-A 1 03-AUG-2004;
Becton, Dickinson and Company; Franklin Lakes, NJ
Location/Qualifiers
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Sequences and methods for detection of hiv-1
Beron. EP 122327-A 1 17-JUL-2002;
Becton, Dickinson and Company (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.8%; Score 13; DB 6; L 100.0%; Pred. No. 7.1e+03; ive 0; Mismatches 0;
         DNA
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Sequence 861 from Patent WO2003097790.
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 Sequence 1 from patent US 6770752. AR575320.1 GI:56576305
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Sequence 1 from Patent EP1223227,
AX474340
                                                                                                                                                                                                                                                                                             /organism="unknown"
/mol_type="genomic DNA"
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Matches 13; Conservative
                                                                                                                                           Unclassified.
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Search completed: March 6, 2006, 00:38:39 Job time: 1169.5 secs
     6 ATGGTAGATACA 17
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Method and reagent for the inhibition of calcium activated chloride
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Patent: WO 0211674-A 1572 14-FEB-2002;
RIBOZYME PHARMACETTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
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41.4%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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Sequence 383 from Patent WO0211674.
AX578545

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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

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/mol_type="unassigned RNA"
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Homo sapiens
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The invention relates to a general primer or primer pair for amplifying and detecting or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes. The general primers are useful for amplifying cervical-neoplasia related HPV genotypes including
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Human Papillomavirus genotype; cervical-neoplasia;
oncogenic high-risk group.
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                                             ABN52768
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31-JUL-2003; 2003KR-00053147.
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Aak13792 Human bon
Abs13626 Human bra
Abs63382 PCBA HH r
Aaa66382 PCBA HH r
Aaa66384 PCBA HH r
Aah61545 PCNA HH r
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Aah61546 PCNA HH r
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd
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                                         OM nucleic - nucleic search, using sw model
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oncogenic high-risk groups and low-risk groups. The general primers are useful for producing amplifying products to DNA of scores of diverse morogenic HPV types and thus detecting the oncogenic HPV types in a sample but also to select cervical carcinoma and its pre-stage lesions at early stage by improving sensitivity according to HPV types. This
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                                                                                                   sequence corresponds to PCR primer used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; primer; detection; diagnosis; amplification;
Human Papillomavirus genotype; cervical-neoplasia;
                                                                                                                                      Sequence 29 BP; 8 A; 7 C; 9 G; 5 T; 0 U; 0 Other;
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The invention relates to a general primer or primer pair for amplifying and detecting or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes. The general primers are useful for amplifying cervical-neoplasia related HPV genotypes including oncogenic high-risk groups and low-risk groups. The general primers are useful for producing amplifying products to DNA of scores of diverse oncogenic HPV types and thus detecting the oncogenic HPV types in a sample but also to select cervical carcinoma and its pre-stage lesions at early stage by improving sensitivity according to HPV types. This sequence corresponds to PCR primer used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New general primer or primer pair, useful for amplifying and detecting, or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
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                                                                                                                                                                                 Human papillomavirus genotype detection PCR primer #12.
                                                                                                                                                                                                             ss; primer; detection; diagnosis; amplification; Human Papillomavirus genotype; cervical-neoplasia; oncogenic high-risk group.
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31-JUL-2003; 2003KR-00053147.
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   8 ACCATAGAGCCACTAGG
                                                                                    ADQ27982 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 ACCATAGAGCCACT 26
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                                                                                                                                                  (first entry)
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALBI-) ALBIOMED CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu K,
                                                                                                                                                                                                                                                                              Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-450746/42.
                                                                                                                                                                                                                                                                                                              WO2004050917-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee S, Kim Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2002
                                                                                                                                                  09-SEP-2004
                                                                                                                                                                                                                                                                                                                                            17-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genotypes.
                                                                                                                    AD027982;
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ID ABN296
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AC ABN296
XX
DT 15-JUL
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                                                                    ADQ27982
                                                     RESULT
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                     gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 14093; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.8%; Score 13; DB 4; Length 93; 100.0%; Pred. No. 7.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe SEQ ID NO: 13783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 93 BP; 29 A; 27 C; 15 G; 22 T; 0 U; 0 Other;
                   marrow expressed exon; gene expression
cancer; leukaemia; lymphoma; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                         26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060B408.
03-AUG-2000; 2000US-0063346.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US000667.
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26-MAY-2000; 2000US-0207456P.
                                                                                                                                                                                    30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                      04-OCT-2000; 2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAGAGCCACTAG 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488900/53.
                   Human; bone marrow microarray; cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2.
                                                                                                            WO200157276-A2
                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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   ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes oligonuclectide libraries for detecting messenger RNAs that populate a (sub-)transcribtome, where the (sub-)transcribtom comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonuclectides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNAs encodes one or more messenger RNAs place variants. The oligonuclectide libraries are useful for detecting mRNAs from a bological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal constitutions of transcriptomes. The libraries may also be used as specialised minical libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue specific tissue under a specific pathological condition; to detect or pathological condition; to detect of a patient suffering from a particular and evaluation of a patient suffering from a particular and evaluates of a transcriptome of a patient suffering from a particular and situation of a patient suffering from a particular survey.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                    Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
 Rat spliced transcript detection oligonucleotide SEQ ID NO:2375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bone marrow expressed single exon probe SEQ ID NO: 14093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13; DB 6; Length 65;
Pred. No. 7.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        Mintz E, Mintz L, Faigler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 65 BP; 17 A; 11 C; 21 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 2375; 47pp; English
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
                                                                                                                                                                                                                                         28-JUL-2000; 2000US-0221607P.
02-MAY-2001; 2001US-0287724P.
                                                                                                                                                                                                    20-JUL-2001; 2001WO-IB001903
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                                                                                                                                                                                                                                                                                                                                      Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
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                                                                                                                                                                                                                                                                                                 (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-257383/30.
                                                                                         Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific genes.
                                                                                                                            WO200210449-A2.
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ID AAK3953
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AC AAK3953
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DT 06-NOV-
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DE Human k
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Rank DR;

Chen W,

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Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                          Claim 4; SEQ ID NO 13617; 634pp; English.
                                                                                                                                                                                                                      The invention relates
                    Hanzel DK,
                                                              WPI; 2002-114183/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2000
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                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
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ID AAA8
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                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; de; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary hatlocytosis; lymphangioleiomyoncosis; Karagener syndrome; pulmonary alveolar proteinnosis; fibrocytic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon probe ORF from lung SEQ ID No 13617.
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                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 13783; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 93 BP; 29 A; 27 C; 15 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyaline membrane disease; open reading frame; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
44.8%; Score 13; DB 4; Le
Best Local Similarity. 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
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                  03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-02346BTP.
27-SEP-2000; 2000US-035359F.
04-OCT-2000; 2000GB-00024263.
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ID ABS13626 standard; DNA; 93 BP.
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30-JUN-2000; 2000US-00608408
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                                                                                                                                                                                                                      WPI; 2001-483446/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nvention
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The invention relates to a spatially-addressation in a sample derived from human lung comprising single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring gene expression in a sample contacting the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably contact acids from enkaryote lung mRNM, to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above mentioned microarray; assigning exons in a single exon of the exons should be assigned to a single exon of the exons should be assigned to a single gene expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising cone of 12011 sequences, mentioned in the specification, or encoded by the expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising analysis, and for identifying exons in a gene; particularly using human cancer, chronic obstructive pulmonary disease ment as astima, lung derived many farter of lung derived many farter or min
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histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis,
Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
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to a spatially-addressable set of single exon
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Pred. No. 7.4e+02;
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13; Conservative
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Disclosure; Page 107; 109pp; English.
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                                                                                                                                             cleaves
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                                                                                                                                       New hairpin and hammerhead ribozyme for inhibiting restenosis, cleave RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
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Pred. No. 2.9e+03;
0; Mismatches 0; Indels
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                                                                                                      Robbins JM;
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                                                                                                                                                                              Disclosure, Page 107; 109pp; English.
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41.4%; Sco
Best Local Similarity 100.0%; Pr
Matches 12; Conservative 0;
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The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RWA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinase CORI, PCNA and Cyclin BI.
Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
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100.0%; Pred. No. 2.9e+03;
ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytckine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule [11] comprising a promoter operably linked to a nucleic acid segment encoding [1]. [1] can have antipsoriatic, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, ophthalmological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. [1] can be used in gene therapy. [1] and [11] are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, virreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn and some and the sequences used in the
                                                                                                                                                                                                                                                                                     Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MNP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antistckling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
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                                                                                                                                                                                                                                              PCNA HH ribozyme binding site SEQ ID NO:3969.
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                                                                                                             AAH61545 standard; DNA; 19 BP
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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [I] which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (WMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid molecule (II) comprising and virucide activities, and seaves RNA encoding cytokine involved in inflammation. (I) can be used claseases such as psoriasis, atopic dermattits, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can disease for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing such as Medolog account as Medolog account as Medolog account as many present search as a such as a
                                                                                                                                                                                                                                                                                                                                                                                                                          Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
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10 GTTACCATAGAG
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                                                                                                                                        RESULT 12
                                                                                                                                                                      AAH61544
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Query Match 41.4%; Score 12; DB 5; Length 19; Best Local Similarity 100.0%; Pred. No. 2.9e+03;

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Gaps ö

Query Match
41.4%; Score 12; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels

Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Length 19;

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a citoravae (I) which claeves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (WMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a conclet acid segment encoding (I). (I) can have antipsoriatic, anticleoratic, anticleborrheic, antidiabetic, antisickling, ophthalmological, cytostatic, antiebeborrheic, antidiabetic, antisickling, cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can disease such as proliferative eye diseases such as diabetic also be used for treating proliferative eye diseases such as diabetic retinopathy, vibreoretinopathy, alckle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing
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                                                                                                                                                                                                                                                                                                                             Human, ribozyme therapy, hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; portiasis; diabetic; retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MWP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scarring such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AAH57577 to AAH62099 represent sequences used in the exemplification of the present invention
    Gaps
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  Indels
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                                                                                                                                                                                                                                                                                            PCNA HH ribozyme binding site SEQ ID NO:3970
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sickle cell retinopathy; ss
                                                                                                                                                                                                                                                        (first entry)
  Conservative
                                      10 GTTACCATAGAG 21
                                                                         8 GTTACCATAGAG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200130362-A2
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12;
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  Matches
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The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (ERTP) or gene; an antibody specific for a CRTP, or cell activated by a CRTP; and antibody specific for a CRTP, or cell activated by a CRTP; and pharmaceutical composition may also comprise a comprise a complex of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNALD, CDH6, CST, ENPP3, FLJ1856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The cancer, bung cancer, breast cancer, prostate cancer, lung cancer, breast cancer, prostate cancer, lung cancer, and esophageal cancer. The present sequence is a concer, stomach cancer, and esophageal cancer. The present sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format directly from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                         Gaps
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                 Score 12; DB 5; L
Pred. No. 2.9e+03;
                                                                            Mismatches
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41.4%; Scc...
100.0%; Pre
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ACL53645 standard; RNA; 21
                                                                            Conservative
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hes 12; Conserv
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                                                                            Matches
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The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (GRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, PLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a cancer interfering RNAs (siRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABGC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for treating cancer.
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                                                                                                                                                                                         Cytostatic, Gene therapy, Vaccine, RNA Interference, cancer, ss, short interfering RNA, gene silencing.
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41.4%; Score 12; DB 14; Length 21;
Best Local Similarity 91.7%; Pred. No. 2.9e+03;
Matches 11; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                        TRPM4 siRNA antisense sequence, SEQ ID 14460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 14460; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Be X, Wei L, Slonim DK, Howes SH;
                                  ACL53388 standard; RNA; 21 BP.
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                                                                                                                 (first entry)
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                                                                           ACL53388;
RESULT 15
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Search completed: March 5, 2006, 22:33:23 Job time : 273.5 secs

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March 5, 2006, 22:21:59; Search time 360 Seconds (without alignments) 666.144 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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SUMMARIES	Description		Sequence 8, Appli	Sequence 9, Appli	Sequence 390726,	Sequence 12, Appl	Sequence 1120, Ap	Sequence 48748, A	Sequence 77937, A	Sequence 100361,	Sequence 587629,	Sequence 590305,	Sequence 203048,	Sequence 295168,	Sequence 403733,	Seguence 968422,	Sequence 84223, A	Sequence 153954,	Sequence 11970, A	Sequence 37797, A	Sequence 48131, A	Sequence 112161,	Seguence 760555,	Seguence 868243,	Sequence 870363,
	ID		US-10-720-424B-8	US-10-720-424B-9	US-10-719-956-390726	US-10-720-424B-12	US-09-969-373-1120	US-10-719-956-48748	US-10-719-956-77937	US-10-719-956-100361	US-10-719-956-587629	US-10-719-956-590305	US-10-719-900-203048	US-10-719-900-295168	US-10-719-900-403733	US-10-719-900-968422	US-10-843-527-84223	US-10-843-527-153954	US-11-036-317-11970	US-11-036-317-37797	US-11-036-317-48131	US-11-036-317-112161	US-11-036-317-760555	US-11-036-317-868243	US-11-036-317-870363
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	å Query Match Length DB		59	24	25	33	96	25	25	25	25	25	25	25	25	25	. 25	25	25	25	25	25	25	25	25
	& Query Match		100.0	58.6	51.7	48.3	48.3	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8	44.8
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Sequence 2375, Ap Sequence 26662, A Sequence 37321, A Sequence 37322, A Sequence 37592, A Sequence 37592, A Sequence 37594, A Sequence 14459, A Sequence 14459, A Sequence 14716, A Sequence 14716, A Sequence 14717, A Sequence 14718, A Sequence 25244, A Sequence 25244, A Sequence 25244, A Sequence 374911, Sequence 374911, Sequence 356087, Sequence 376087, Sequence 360488, Sequence 468309, Sequence 468309,	FOR DETECTING DIVERSE GENOTYPES OF	Length 29; Indels 0; Gaps 0;
US-09-908-975-2375 US-09-864-761-26662 US-10-751-736-37321 US-10-751-736-37591 US-10-751-736-37591 US-10-751-736-37594 US-10-751-736-37594 US-10-751-736-37594 US-10-84-918-14458 US-10-84-918-14459 US-10-84-918-14416 US-10-84-918-14717 US-10-84-918-14717 US-10-84-918-14717 US-10-719-956-25244 US-10-719-956-25244 US-10-719-956-356087 US-10-719-956-356087 US-10-719-956-356087 US-10-719-956-356087 US-10-719-956-356087 US-10-719-956-35688 US-10-719-956-35688 US-10-719-956-35688 US-10-719-956-35688	RESULT 1  US-10-720-424B-8  Sequence 8, Application US/10720424B  Sequence 8, Application US/10720424B  Sequence 8, Application OS US20040248085A1  SERNEAL INFORMATION: APPLICANT: ALBIOMED CO., LTD APPLICANT: Kim, Yeon-Soo APPLICANT: Kim, Yeon-Soo APPLICANT: Kim, Seung-Wa APPLICANT: Kim, Seung-Wa APPLICANT: Kim, Seung-Va APPLICANT: Cha, Kwang-Yul APPLICANT: Cha, Wang-Yul APPLICANT: Cha, Wang-Yul APPLICANT: Cha, Ung-Ja APPLICANT: Cha, Wang-Yul APPLICANT: Cha, Wang-Yul APPLICANT: Cha, Ung-Ja TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR I TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS  CURRENT APPLICATION NUMBER: US/10/720,424B  CURRENT APPLICATION NUMBER: KR10-2002-0075370  PRIOR FILING DATE: 2003-11-29  PRIOR FILING DATE: 2003-131  NUMBER OF SEQ ID NOS: 16  SEQ ID NO SEQ ID NOS: 16  LENGTH: 29	ore 29; DB 8; Leed. No. 1.2e-07; Mismatches 0; ACTAGG 29 ACTAGG 29 ACTAGG 29
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Application US/107 Application US/107 NWATION: ALBIOMED CO., LTD Lee, Sang-Wha Kim, Seung-Vool Kim, Seung-Vool Kim, Seung-Vool Ko, Jung-Jeol K	TYPE: DNA ORGANISM: Human Papillomavirus -10-720-424B-8 Query Match Best Local Similarity 100.0%; Score 29 Best Local Similarity 100.0%; Pred. No Matches 29; Conservative 0; Mismatch I GCGTCAGACGTTACCATAGAGCCACTAGG
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-10-720-424B. Sequence 8, 1 SEQUENCE 8, 1 SEQUENCE 1 INCOLUMENT 1 APPLICANT: 1 APPLIC	; TYPE DNA ; ORGANISM: Human Papill US-10-720-424B-8 Query Match Best Local Similarity Matches 29; Conserva OY  1 GCGTCACAGGT  Db 1 GCGTCACAGGT  INCOTTO CONSERVA  RESULT 2 US-10-720-424B-9 ; Sequence 9, Application ; Publication No. US20040; ; APPLICANT: Lee, Sang-1 ; APPLICANT: Kim, Yeon

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MESULT 6
US-10-719-956-48748/C
US-10-719-956-48748, Application US/10719956
; Sequence 48748, Application US/10719956
; Publication No. US20040146910A1
; GRUERAL INFORMATION:
; APPLICANT: KUE Mei Zhou
; TITLE REFERENCE: 3527.1
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT PILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; ROWHER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1120, Application US/09969373
; Sequence 1120, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; TITLE OF INVENTION: Soybean SSRs and Methods of Concrete String Data: 2001-10-02
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR PAPLICATION NUMBER: US 09/760,427
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 33; 1.7e+02;
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FILE REFERENCE: NEITOO18
CURRENT APPLICATION NUMBER: US/10/720,424B
CURRENT PILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: KR10-2002-0075370
PRIOR PILING DATE: 2002-11-29
PRIOR APPLICATION NUMBER: KR10-2003-0053147
PRIOR PILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
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48.3%; Score 14; DB
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 TTACCATAGAGCCA 76
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APPLICANT: Lee, Sang-Wha
APPLICANT: Kim, Yeon-Soo
APPLICANT: Yu, Kang-Yeol
APPLICANT: Kim, Seung-Vol
APPLICANT: Cha, Kwang-Yul
APPLICANT: Cha, Wang-Yul
APPLICANT: Cha, Wang-Yul
APPLICANT: Cha, Wang-Jae
TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
                                                                           APPLICANT: KO, JUNG-Jack
TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
FILE REFERENCE: NEITOOL8
CURRENT APPLICATION NUMBER: US/10/720,424B
CURRENT FILING DATE: 2003-11-24
PRIOR FILING DATE: 2003-11-29
PRIOR FILING DATE: 2002-11-29
PRIOR FILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 16
SOFTHARE: PALENTIN VERSION 3.2
LENGTH: 24
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.6%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.7%; Score 15; DB 100.0%; Pred. No. 43; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 390726, Application US/10719956 Publication No. US20040146910A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 ACCATAGAGCCACTAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ACCATAGAGCCACTAGG 24
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US-10-719-956-390726
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Best Local Similarity 100.C
Matches 15; Conservative
                                Kim, Seung-Jo
Cha, Kwang-Yul
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US-10-719-956-390726/c
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LENGTH: 25
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US-10-720-424B-12
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  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 35.77
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 06/427,836
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 567629
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11.20
PRIOR PILING DATE: 2002 11.20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 590305
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
44.8%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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TITLE OF INVENTYON: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR PILING DATE: 2002 11 20
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  Sequence 587629, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
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; Sequence 203048, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-719-956-590305
US-10-719-956-590305
Sequence 590305, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-587629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Rattus norvegicus
US-10-719-956-590305
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Best Local Similarity
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Publication No. US20040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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; Bublication No. U320040146910A1
; GENERAL INFORMATION:
; AFPLICANT: Xue Mei Zhou
; TITLE OF INFORMATION:
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR PILING DATE: 2003-11-20
; PRIOR PILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                                                                  Length 25;
                                                                                                                                                   Indels
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44.8%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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7.2e+02;
                                                                                             Query Match
44.8%; Score 13; DB
Best Local Similarity 100.0%; Pred. No. 7.5
Matches 13; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 7.5
Matches 13; Conservative 0; Mismatches
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-48748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-100361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-77937
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US-10-719-956-587629/c
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US-10-719-956-77937
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US-10-719-900-295168/c

is Sequence 295168 Application US/10719900

publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

ITILE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3520.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

FRIOR PILING DATE: 2003-11-20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 403733
LENGTH: 25
                                                         44.8%; Score 13; DB 8; Length 25; 100.0%; Pred. No. 7.2e+02; tive 0; Mismatches 0; Indels
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s 0; Indels
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Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR FILING DATE: 2002-11.20
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                                                                               Best Local Similarity 100.0
Matches 13; Conservative
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                                                                                                                                                5 CAGAGGTTACCAT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus
US-10-719-900-295168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-403733
; ORGANISM: Mus musculus
US-10-719-900-203048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
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US-10-719-900-968422 ; Sequence 968422, Application US/10719900

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; Sequence 8423, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
    APPLICANT: Michael Mitmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; RIOR APPLICATION NUMBER: 60/469,545
; RIOR APPLICATION NUMBER: 60/469,545
; RIOR PRING DATE: 2003-06-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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GENERAL INFORMATION:
GENERAL INFORMATION:
FAPPLICANT: Xue Mei Zhou
TITLE OF INVENTION:
CURRENT APPLICANTON WEATHOR of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT FILING DATE: 2003-11-20
PRIOR FILING DATE: 2003-11-20
PRIOR FILING DATE: 2003-11-20
SPRIOR FILING DATE: 2003-11-20
SPRIOR FILING DATE: 2003-11-20
SPRIOR FILING DATE: 2002-11-20
SPRIOR FILING DATE: 2003-11-20
SPRIOR FILING DATE: 
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Pred. No. 7.2e+02;
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-843-527-84223
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Best Local Similarity
Matches 13; Conserv
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US-10-843-527-84223/c
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1195364

Sequence

Sequence 1192502 Sequence 1255833

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence

Sequence

Sequence 1306392 Sequence 1472078

Sequence Sequence Sequence

Sequence

Sequence

Sequence:

Run on:

Searched:

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APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Acreall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-01-14
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                      44.8%; Score 13; DB 10; 76.9%; Pred. No. 1.8e+02; iive 3; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1039686, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1039686, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:
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APPLICANT: Khvorova, Anastasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1039686
LENGTH: 19
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Best Local Similarity 76.9
Matches 10; Conservative
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US-11-101-244-1039686
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Sequence 49, Appl
Sequence 1107332,
Sequence 79718, A
Sequence 79729, A
Sequence 79759, A
Sequence 79759, A
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Sequence 1009686,
Sequence 210096,
Sequence 417792,
Sequence 105826,
Sequence 105834,
Sequence 105834,
Sequence 307731,
Sequence 307731,
                                                                                                                                       5, 2006, 22:22:58; Search time 449.5 Seconds (without alignments) 141.451 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications NA NWW: *

(cgn2_6/prodata/1/pubpna/USOB NEW PUB.seq:*

(cgn2_6/prodata/1/pubpna/USO6_NEW PUB.seq:*

(cgn2_6/prodata/1/pubpna/USO7_NEW PUB.seq:*

(cgn2_6/prodata/1/pubpna/PCT_NEW PUB.seq:*

(cgn2_6/prodata/1/pubpna/USO9_NEW PUB.seq:*

(cgn2_6/prodata/1/pubpna/USO9_NEW PUB.seq:*

(cgn2_6/prodata/1/pubpna/USO9_NEW PUB.seq:*

(cgn2_6/prodata/1/pubpna/USO1_NEW PUB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-083-784-1039686
US-11-121-849-235837
US-11-121-849-235837
US-11-121-849-417792
US-11-136-527-105827
US-11-136-527-105834
US-11-136-527-105834
US-11-136-527-105835
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US-11-136-527-105835
US-11-136-527-105835
US-11-175-885-37597
US-11-173-887-37
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US-10-310-914A-811205
US-11-101-244-79718
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US-11-101-244-79729
US-11-101-244-79757
US-11-101-244-79763
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                                                                                            - nucleic search, using sw model
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29
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Match Length
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Perfect score:
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Result No.

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US-11-121-849-417792/C

US-11-121-849-417792/Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT PILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR PILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Sequence 10526, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-04100 (AMI01086)
CURRENT APLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 105826

LENGTH: 25
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PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 235837
LENGTH: 25
                                                                                                                                                                                                                   44.8%; Score 13; DB 12; Length 25; 100.0%; Pred. No. 1.8e+02;
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100.0%; Pr
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-235837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapien
US-11-121-849-417792
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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Publication No. US20050272080A1
GENERAL INPORMATION:
APPLICAMT: John Palma
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION NUMBER: US/11/121,849
TOTRENT APPLICATION NUMBER: US/567,949
PRICE FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    % Sequence 235837/c
; Sequence 235837, Application US/11121849
; Sequence 235837, Application No. US20050272080A1
; Sequence 235837, Application No. US20050272080A1
; GENERAL INFORMATION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded () TITLE OF INVENTION: Microarrays
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
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Pred. No. 1.8e+02;
3; Mismatches 0; Indels
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44.8%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
                       APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 76.9%;
Matches 10; Conservative
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SOFTWARE: Proprietary
     Reynolds, Angela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-083-784-1039686
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US-11-121-849-210096
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US-11-121-849-210096
                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1039686
LENGTH: 19
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LENGTH: 25
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Gaps

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APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE OF INVENTION: 0.0186-04100 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
LENGTH: 25
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APPLICANT: Wounts, William M

TILL OF DEADLE WILLIAM M

TILL OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

NUMBER OF SEQ ID NOS: 362303

SOFTWARE: Patentin version 3.2
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APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.8%; Score 13; DB 12; 100.0%; Pred. No. 1.8e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13; DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
  Sequence 105835, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
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; Sequence 307733, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
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100.0%; Pre
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Best Local Similarity 100.
Matches 13; Conservative
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Matches 13; Conservative
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ORGANISM: Artificial
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LENGTH: 25
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FUDLication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVERTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE OF INVERTION Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

NUMBER OF SEQ ID NOS: 362830

SEQ ID NO 105827

LENGTH: 25

LENGTH: 25
       Gaps
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AMJ01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
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44.8%; Score 13; DB 12; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0;
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44.8%; Score 13; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 13; Conservative 0; Mismatches
  Mismatches
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GENERAL INFORMATION:
APPLICANT: Wyeth
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SOFTWARE: Patentin version 3.2
SEQ ID NO 105834
LENCTH: 25
                                                                              1 TACCATAGAGCCA 13
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                                                 12 TACCATAGAGCCA 24
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  13; Conservative
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ORGANISM: Artificial
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                                                                                                                                                                                         US-11-136-527-105827
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US-11-136-527-105835
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Publication No. US2006002954A1

GENERAL INFORMATION:

APPLICANT: LAO, KAI QIN

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/11/173,887

CURRENT FILING DATE: 2005-06-30

PRIOR PILING DATE: 2004-06-30

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PARENTING PATE: 2004-06-30

SOFTWARE: PATENTING NOW: 50

SOFTWARE: PAT
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Sequence 37597, Application US/11175859

Publication No. US20060024715A1

GENERAL INFORMATION:

APPLICANT: Affymetrix, Inc.

APPLICANT: Liu, Guoying et al.

TITLE OF INVENTION: Method of Analysis of Human Polymorphism

FILE REFERENCE: 3690.1

CURRENT APPLICATION NUMBER: US/11/175,859

CURRENT FILING DATE: 2005-07-05

PRIOR APPLICATION NUMBER: US 60/585,352

PRIOR APPLICATION NUMBER: US 60/585,352

PRIOR PILING DATE: 2004-07-02

SOFTWARE: PatentIn version 3.2

SEQ ID NO 37597

LENGTH: 50
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44.8%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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ches 0;
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PRIOR APPLICATION NUMBER: US 60/574,294 PRIOR FILING DATE: 2005-05-26 NUMBER OF SEQ ID NOS: 362830 SOFTWARE: PatentIn version 3.2 SEQ ID NO 307741 LENGTH: 25
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US-11-175-859-37597
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US-11-173-887-37
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Sequence 1107332, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof
                                                                                                                                                                                                                                                           Sequence 49, Application US/11173887

Sequence 49, Application US/11173887

Publication No. US20060029954A1

GENERAL INFORMATION:

APPLICANT: LAO, KAI QIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING NUCLECTIDES IN

TITLE OF INVENTION: POLYNUCLECTIDE SEQUENCES

FILE REFERENCE: 375461-017US

CURRENT APPLICATION NUMBER: US/11/173,887

CURRENT APPLICATION NUMBER: 60/584,643

PRIOR FILING DATE: 2005-06-30

NUMBER OF SEQ ID NOS: 50

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 49

LENGTH: 63
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     Length 63;
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44.8%; Score 13; DB 9; Loudous; Pred. No. 1.8e+02;
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v 100.0%; Pred. No. ...
0; Mismatches
               100.0%; Prec. ... 0; Mismatches
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 13; Conservative
                                                 13; Conservative
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  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                   US-11-173-887-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
                                                    Matches
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Search completed: March 5, 2006, 22:48:30 Job time: 450.5 secs

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Human Human

March

Run on:

OM nucleic

Scoring table:

80

Minimum I Maximum I

Title: Perfect score:

Sequence:

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AY863160 Human pap
AY863161 Human pap
AY863162 Human pap
AY863163 Human pap
AY863164 Human pap
AY863165 Human pap
U89349 Human papil
U31790 Human papil
         AX452915 Sequence CS103057 Sequence AR047985 Sequence AR059325 Sequence CQ815809 Sequence AY101598 Human pap AY863157 Human pap
                                                                                                                                                                                                                                         CS073239 Sequence
AY262282 Human pap
X05015 Human papil
X62843 Human papil
X77858 Human papil
                                                                                                                                                                                                                                                                                                                                                                         DQ003076 673 bp DNA linear VRL 15-AUG-2005
Human papillomavirus type 54 nonfunctional L1 gene, partial
sequence.
                                                                                                                                                                                                            AF436129 Human pap
CS073242 Sequence
                                                                                                                                                                                                                                    D90400 Human papil
DQ003070 Human pap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu, X., Ren, J. and Ma, R.Z.
Direct Submission
Submitted (08-APR-2005) Institute of Genetics and Developmental
Biology, Chinese Academy of Sciences, A5 Datun Raod, Chaoyang
District, Beijing 100101, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clinical
                                                                                                 AY863158 F
AY863159 F
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Human papillomavirus - 54
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mu,X., Ren,J., Ran,D. and Ma,R.Z.
Detection of HPV types in cervical brush samples of
patients in Beijing and other Northern China cities
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .673
/organism="Human papillomavirus - 54"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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/note="nonfunctional L1 due to mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27.4; DB 13;
Pred. No. 0.98;
0; Mismatches 1;
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HPVT13DNA
           AX452915
CS103057
AR047985
AR059325
CQ815809
AY101598
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CS073239
AY262282
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AY863162
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HPU89349
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CS073242
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Best Local Similarity 96.6%; Pre
Matches 28; Conservative 0;
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                                                                                                 Alphapapillomavirus.
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DQ003076.1
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JOURNAL
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ORIGIN
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AA520205 Human pap
117042 Sequence 53
BD017550 Short-cha
A91822 Sequence 2
AR216808 Sequence
AR216809 Sequence
BD023226 Papilloma
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AF070938 Human pap
U40822 Human papil
U37488 Human papil
AF436130 Human pap
AF020905 Common ch
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DQ003068 Human pap
DQ003075 Human pap
DQ003078 Human pap
                                                                      5, 2006, 21:52:50 ; Search time 907 Seconds (without alignments) 1817.486 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                       11766282
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                 5883141 seqs, 28421725653 residues
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                           gatggtgatatggtagatacaggatttgg 29
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                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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DQ003068
DQ003075
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AF436130
AF020905
AF419318
AJ620205
I17042
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A91822
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BD023226
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
                                                                                                                   US-10-720-424B-1
29
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gb\_sy:\* gb\_un:\* gb\_vi:\* gb\_htg:\* gb\_pl:\*

Length

Query

Result

7759 7887 7889 7966 7975 38 386 386 386 386

gb\_ro:\* gb\_sts:\*

9: 10: 11: 12:

gb\_pat:\* gb\_ph:\* gb\_pr:\* gb\_om:\*

gb\_in:\* gb\_env:\*

**ba:**\* GenEmbl:\*

Database

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Gaps

ORGANISM

KEYWORDS SOURCE

AUTHORS

TITLE

REFERENCE

TITLE JOURNAL

FEATURES

REFERENCE AUTHORS JOURNAL PUBMED

DEFINITION

RESULT 2 AF070938

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ACCESSION VERSION

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NEGONRVNVANDYVRADSCALELITSVI
ODGDNVDTGFGAANDALDLQPTKSDVPLDI CNTTCKYPDYLQNAADPYGDRLFFYLRKE
OMFARHFRAGTVGEDI PQDLYI KGTTRSTLANA I Y FNT PSGSL VSSETQLFNKPFW
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FDLQA PGCANAT CWGNQLFYTH STUMYVCAPFGSPSQSPSYTVSSDYK KQYRHVEE
FDLQA PGCANAT CWGNQLFYTH THAND TULEBWN FGLTPPPNGTLEDTYR VVGSQA IT
CQKPTPDRAKFNPFYANLS FWEVNLKEKFSSELDQYPLGRKFLLQTGVQARSSVRVSKK
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QLTQAYQIVTCCGVCNRSLRLVVQCTGPDINNLHTLLLGTLNLVCPLCAPKT"
                                                                                                                                                                                    (HPV), HPV type 74, found in
                                                                                                                                                                                                                                                                                                                                                      Longuet, M., Cassonnet, P. and Orth, G.
Direct Submission
Submitted (17-NOV-1995) Michele Longuet, Laboratoire des
Papillomavirus, Institut Pasteur, 25 Rue du Dr Roux, Paris 75015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Human papillomavirus type 74
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
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Longuet, M., Caesonnet, P. and Orth, G.
A novel genital human papillomavirus (HPV), I immunosupressed patients
J. Clin. Microbiol. 34 (7), 1859-1862 (1996)
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/gene="E7"
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Matches 28; Conservative
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/gene="E6"
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/gene="E6"
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/gene="E7"
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/gene="L1"
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PLDLCNTKSKYPDYLGMAAEPYGNSLFFFLRREQMFVRHFFNKAGTTGDAVPQDLYIA
                                                                                                                                                                                       AF070938 1546 bp DNA linear VRL 30-SEP-1998
Human papillomavirus late major capsid protein (LJ) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGNRAKI AGS I YYSTPSGSLVTSDSQLPNKPLÄMQKAQGHNNGI CFGNQVFVTVVDT
TRSTNLTLCASTESVLPTYDNTKFKBYLRHABEPDLQP I PQLCI ITLAPEVMYY I HT
MDASLLEDMNFGVS PPSHGSLEDTYR PLANKAI TCQKNVP PKAKEDPYKNYTFMDVDL
TERF8DAQLTQPPLQRKKVYMQAGIR PR PKLKSGRRAAPSSSSAPASKRKKTKR.
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U40822.1 GI:1491796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Yocov, M.V.
Direct Submission
Submitted (05-UNN-1998) Cancer Center Charles Bruneau, Hospital
Ste-Justine, 3175 Cote Ste-Catherine, Montreal, QC H3T 1C5, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JC9813-A putative novel human papillomavirus identified by PCR-DS Biochem. Biophys. Res. Commun. 250 (1), 63-67 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feoli-Fonseca, J.C., Oligny, L.L., Filion, M., Simard, P., Russo, P.A. and Yotov, W.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feoli-Fonseca, J.C., Oligny, L.L., Filion, M., Simard, P., Russo, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Human papillomavirus"
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/db xref="texon:10566"
/note="identified in 1997 in a cervical biopsy from a 38.year old English Canadian woman, HIV-positive since 9. 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="late major capsid protein"
|protein id="AAC62011.1"
|db_xref="G1:3676539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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96.6%; Pred. No. 0.9;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGGTGATATGGTAGATACAGGGTTTGG 618
                  530 GATGGTGATATGGTAGATATAGGATTTGG 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus
Viruses; dsDNA viruses, no RNA
unclassified Papillomaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                         AF070938
AF070938.1 GI:3676538
                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="L1"
8. .1516
/gene="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 1546)
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Best Local Similarity 96.6
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1546
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gene

CDS

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Gaps

DEFINITION

HPU40822 RESULT 3

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ORIGIN

ACCESSION VERSION KEYWORDS SOURCE

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HPYFKOCKTNIKOS IPKVSGYQYRVERVQLDDPNKFGLEDBSLYNDFTQRLWAACTGV
WCRQPLGLGLGGHPLLNKLDDTBNAPKYVGAGADNRBNVSMDYKQYQLCTLGCTPV
IGEHWAKGNLCTPNTLAAGDCPPLELLNWSY IQDGDWVD IGFGAMDFKTLQTSKSEVEL
DVATGSICKYPDYLKNABAGDCSPFEYLRREQMFVRHMLNRAGTMGBEVPNDLY IKKS
SGNLDSSIYAATPSGSMYTSEYQIFNKPYWLQRAGGQNNGICWGNOVFLTVVDTTRST
NTLCATASTQDSFNNSDFREY IRWESPDAGCFIPGLCTITTADWAXIHGNNPTIL
BUNNFGITPPATSSLEDTYRFVOXGAJACQNGNAPAKEKEDPYSKFNFWTVDLKERFF
SDLDQFPLGRKFLLQAGLRARPRLRPVKRAAPSSSKGTARKAKTKR"
                                                                                                                          /protein_id="AAA79190.1"

/db_xref="G1:1017786"

/db_xref="G1:101786"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mowvFilmmontkcimmilkrkhlsmgnmdsgrcvmaaasffll
hlylvpkrhcqypllallatlatedopiphhypttpokosrarrilenelestaqtsnhta
potpmavtttgtsvtittrkdgtqvvvtlhl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVSLVEESSVVDVGAPTPTI PSQGGFEIATSSDATPALLDVTSTTTPIRVSITSHDNP
IYTEPSLLDPPPPVQMDGRVLVSTSTLQSSTAENIPMDTFIIMQDHIGTTTSTPIPRP
PARPRLGLYSRALQQVPVQDPAFLQQPSSLITYDNPVYEGNPDVTLHFEQPTIHNAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAFMDIFALHRPALTTRRGVVRYSRVGDRATLHTRSGLQLKPRVHFFQDLSPIAHVPE
EIELHPLISANNTSINNGLYSDIYDDYADTDFADTGGFSSSTVSHSSVQTALQTTSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQYGNTTVPLTASSPYTPIPTSFRPSSGHTPFVPARPIFPQTPIAVNGGDFYLHPSYT
YVRKRRKRFPYFLADGYVAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRWGSMGVFFGGLGIGTGSGTGGRTGYIPLGRPSTTLEPGPPVRPAGAVETVAPSDPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MAKARAPRRKRASATQLYQTCKASGTCPSDVIPKVEGTTIADQ"
                           note="putative; ORF B2 from bp 2644 to 3774"
/codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="putative; ORF L2 from bp 4200 to 5627"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="putative; ORF L1 from bp 5422 to 7107"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="putative; ORF E4 from bp 3134 to 3538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; DB 13;
0.76;
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/product="major capsid protein"
/protein_id="AAA79193.1"
/db_xref="GI:1017789"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'codon_start=1
'product="minor capsid protein"
                                                                                                  /product="regulatory protein"
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA79192.1"
/db_xref="GI:1017788"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein id="AAA79191.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGGTGATATGGTAGATACAGGATTTGG
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/gene="L2"
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/gene="E4"
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/gene="E4"
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/gene="L1"
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/gene="L2"
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/gene="L1"
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Best Local Similarity
Matches 28; Conserv
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AF436130
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/framslation="MSATEPHTOQPRTLADLCKVCNIPMHSLQLPCAFCKKTVCTABI
AAPQYROLFVWRHGFHAACALCLELHGQINYRHRDRACLWETVEQEGKPLEBIF
RCWLCHKPLCNVFKQRHYDYNRRHCVRGYWKGRCLHCWKP"
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QAFKVLSQCGGVCCKTVRLCVYSTHTGIRVLQELLHQDALQIVCPTCASRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MADDNQTEEEGTGCNGWFFVEAIVERKTGDIISDDEPEDVEDSG
LDMVDFIDDSSQQVEGQENPQALLHAQQLQADVEAVQQLKRKYIGSPYVSPVANSEPC
VEKDLSPRLGAISLGRRSAKAKRRLFDKAQPPPNGHTDVEAAVEVNTEGTDETETDQV
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DSQFDLSKWQWAYDHNY I DDS I IALEYAKLAD I DENAAAFLGSNCQAKYVKDCGTWC
RHY IRAQMOMTWSQWI KHRCDLVEEEGEWKEI VRFLARQTVDFI SFWIALKQFLQGI
PKHYI LLI YQPPOTGKSNFAMSLI SFROWCETSYNSSSHFWLDFI SFWIALDDAT
TQCWNYNIL IYRNALDGSNPWCFDRKHRAMOQTKCPPLI YTSNINASTDDRWRY IHRSKY
KCFFCPPNR FPFDSNGNPVYDLSNKNWKSFFKRSWSRLALNDNDHEEEBNGDFSNITFRC
                                                                   VRL 06-DEC-1999
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WVIAAFG1YHG1TDGFKTLLEPHCLYGH1QMLTCRWGMVLLLLTRFRCGKNRLTVSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (03-OCT-1995) Andrew Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 97501 USA
HPV-54 was first isolated from a patient with condyloma acuminata.
Location/Qualifiers
                                                                                                                                                                                                                     Human papillomavirus - 54
Human papillomavirus - 54
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="putative; ORF E6 from bp 7708 to 536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="putative; ORF El from bp 795 to 2729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="putative; ORP E7 from bp 512 to 823"
                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organiem="Human papillomavirus - 54"
|mol_type="genomic DNA"
|db_xref="taxon:333766"
|lo2. .536
                                                         HPU37488 7759 bp DNA lind
Human papillomavirus type 54, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t="transforming protein"
n_id="AAA79187.1"
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protein_id="AAA79188.1"
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protein id="AAA79189.1"
db_xref="GI:1017785"
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/gene="E2"
2671. .3774
                                                                                                                                                               U37488.1 GI:1017782
                                                                                                                                                                                                                                                                                                                        Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 7759)
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/gene="El"
828. .2729
/gene="El"
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/gene="E6"
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/gene="E7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db xref="
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                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                        DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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RESULT 4
HPU37488
                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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FEATURES
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Gaps

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Indels

A. 18344

Length 7759;

DEFINITION

REFERENCE AUTHORS TITLE

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

CDS

JOURNAL

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/ Cranslation="MAHSRARRKRASATQLYQTCKVSGTCPSDIIPKIEHNTIADQI
IKWGSLGVFFGGLGIGTGGRTGYIPLOSAPRDDIPSGPAARPPIIVDTVGFBGDP
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ATRPRIGLYSRALHQVQVTDPAFLSSPQRLITFDNPVYEGEDVSLOFGHNTIHNPPDD
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AEEIELHPLVAHAQDSSGLFDIYAEPDLEVWEEPVPLSFSTSTPFGRSAGATGWTRYDT
VPLSLFGODMFTQPRGPDIMFPTASSTTPYSSPVTPALFTSTPFGRSAGATWGNTY
VRINTHPLFFTDVAA"
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TSPTIPTKHALVTYANBQQRQOFLDTVRLPTISYKLGYMSLQLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / LTAIN LALL OID = "MYLHFIYIHHGILHANAVNMFPCFLQMWRPSDNQYYPPPAPVS
KVITTDAYVTRTN I FYHASSSRLLAYGNPYFPI KQYNKTYVPKYSGYOFRVFKYLLDD
KVITTDAYVTRTN I FYHASSSRLLAYGNPYFPI KQYNKTYVPKYSGYOFRVFKYLLDD
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ODGDNNDTGFGANNFRELQPLKSDYPLDICKYTPCKYPDYLQMAADPYGDRLFFYLRKE
QMFARHFFNRAGTVGEDIPQDLYIKGTTRGTLANAIYFNTFSGSLLVGSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQKAQGHNNGI CWGNQLFVTVVDTTRSTNMTVCAPTTQSPPAATYTSTDYKQYMRHVE
BFDLQFI FOLCSI TAZBVNAY I HTWNPTVLEDWNFGLTPPPDKGTLEDTYRYVOSQAI
ACQKPTPDKAKPNPYANLSFWEVNLKEKFSSELDQYPLGRKFLLQTGVQARSSVRVGK
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cktypllgilhtpppppplhrppqcplpppritytrpvkdpedvpptptppttp
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SILVLTLILYLLEWLLLTSALQFYTLTLCVCYLPAFSLHLYILHNLE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="putative minor capsid protein L2"
protein id="AAO15461.1"
db_xref="G1:27462490"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative major capsid protein L1"
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/db_xref="G1:27462491"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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/db_xref="G1:27462489"
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/protein_id="AA015459.1"
/db_xref="G1:27462488"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27.4; DB Pred. No. 0.76; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6170 GATGGTGATATGGTAGATACAGGCTTTGG 6198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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                                                                                                                                                                                                                                                                               codon_start=1
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/gene="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3762. .4037
/gene="E5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.5%;
Best Local Similarity 96.6%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4210. .5604
/gene="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3762. .4037
/gene="E5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5513. .7099
/qene="L1"
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/gene="L1"
                                                                                                                                                                       3060. .3485
/gene="E4"
                                                                                                                                                                                                                        3060. .3485
/gene="E4"
                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MarnTGTECTGCSGWFLVEAIVEHTTGQQISEDEDETVEDNGSD
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GROTGERETWYQTSDTQQQTRATTRILELLCKCHOVRATLLGKRECYGLSYTDLRQF
KSNKSTCGHWVVAAFGVHHSVADAFQNLIQPVTTYSHIQWLTNAMGMYLLALLTFKVN
RYTTYRAMLATLLIN PEDHMLIEPRYK GSTYAALWRRSSENASIVGOTPWITR
CYIUBHGIADNQFALADWYQMAYDNDLCDESEIAPDYAGRADIDANRAFLNSNCQAK
YVKDCATMCKHYKNAEMKKQMNHKQWIHYRSSKVEEAGNWKPIVQFLKHQNIEFIPFES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLKLWILHGTPKKNCI AI VOPPDIGKSCFGMSLI KFLGGTVI SYVNSSSHFWLOPLCNA
KVALLDDATQSCWYJ DTYMRNILDGNPMSLI KFLGGTVI SYVNSSSHFWLOPLCNA
KVALLFSRVSVFTFPNPFPFDRNGNAVYDLCESNWKCFFTRLSASLDI QNSEDEDDGD
NSQAFRCVPGTVVRTV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="METIAKHLDVCQEQLLELYEENSNNLEKHIQHWKCVRHESVLLH
                   VRL 02-JAN-2003
                                                                                                                                                                                                                                                                                                                                                      Unpublished

2 (bases 1 to 7887)

Burk, R.D. and Terai, M.
Direct Submission
Submitted (22-00T-2001) Microbiology & Immunology, Albert Einstein
College of Medicine, 1300 Morris Park Avenue, Bronx, New York, NY
                                                                                                                                                                                                                           Alphapapillomavirus.
I (Dases 1 to 7887)
Terai,M. and Burk,R.D.
Cervical HPVs in Evolution; Genomic sequence of AE10, a Subtype of
AF436130 7887 bp DNA linear VRL 02-
Human papillomavirus type 74 subtype AE10, complete genome.
AF436130
                                                                                                                                              Human papillomavirus type 74
Human papillomavirus type 74
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .453
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| protein id="AA015455.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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protein_id="AAO15457.1"
db_xref="GI:27462486"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           id="AAO15456.1"
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                                                                                             AF436130.1 GI:27462483
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/gene="E2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          721. .2643
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/gene="E7"
429. .716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="E7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="E2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10461, USA
                                                                                                                                                                                                                                                                                                                                   HPV74
                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
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gene

CDS

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TLAGATYTVPSSVSEECVQAPPSKRORGPSOSAGKTOHTCNIVCDTDCATLDSANNI
NNNSYSSNNGRNNSYCTGTPIVQLQGDSNNLKCFRYRLHSNYKHLFFACISTWHWTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAFMDI IRLHRPALTSRRGVVRFSRIGGRGSMYTRSGKHIGGRVHFFTDISPISADAQ
DIELQPLVAAAQDDSDLFDIYVDPDTTPVAVDNIPSANSTLFIKSSIFDTSWGNTTIP
LSLPNNI FVQPGPDILFPTTPAVPPYGPVISPLPVGPVFISGSEFYLHPSLYFARKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mmrpsdnklyvpppapvskvlttdayvtrtkifyhasssrllav
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LTPPKHCFKKQGKTVEVKYDCNAENTMHYVLWKYIYVYNTEKEIMLKVKGMVDYKGLY
                                                                                                                                                                                   YMMEQCKTYYVDFEKEAKQYGKTLQWEVCFDSTVICSPASVSSTVQEVSNAGPTSYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KWGSLGVFFGGLGIGTGSGTGGRTGYVPLESAPRPAIPFGPTARPPIVVDTVGPTDSS
IVSLVBDSAIINGGASDLVPSIHGGPSISTSBSTTPAILDVSITTHNTTSTSIFRNPA
PAEPSIVQSQPSVEAGGHLTGTFTSTISPHSVEEIPLDTFIVSSSNSNPASSTPVPT
TVARRRLGIXSKALHQVQYTDPAFLSSPQRLITFDNPVYBGEDISLHFBNSIHBPPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLGEHWGKGKQCSGVSVQDGDCPPLELVTSVIQDGDWVDTGFGAMDFAELQSNKSDVP
LDICTSTCKYPDYLQMAADPYGDRLFFYLRKEQMFARHFFNRAGTVGEQIPDELFVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTSRATVSSNIYFNTPSGSLVSSBAQLFNKPYMLHKAQGHNNGICWGNTLFVTVVDTT
RSTYMTVCASTTSSBAATTASBYKQYMRHVBBEDLQFIFQLTIKATABLMAYIHTM
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                                                                                                           /translation="METLAKHLDACOEOLLELYEENSNELKKHIOHWKCVRYENVLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'translation="MAHSRPRRRRASATQLYQTCKASGTCPDIIPKVEQNTLADKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAB71710.1"
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                                                        /protein_id="AAB71707.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein id="AAB71709.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVTTDGTTVTVLVHL"
                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1/product="E4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
product="L2"
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Best Local Similarity 96.6'
Matches 28; Conservative
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VLLRFKVNKNRCTVARTLATLLNIPEDHMLIEPPKIQSSVAALYWFRTSISNASIVTG
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WLQPLCNAKVALLDDATQSCWGYMDTYMRNLLDGNPMSIDRKHKSLALIKCPPLLVTS
                                                     VRL 01-0CT-1997
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                                                                                                                                                                                                                                                                                                                                 Scinicariello, F., Soza, I., Brasky, K.M. and Hilliard, J.K.
DNA sequence of a novel papillomavirus (CCPVI) from an outbreak of
focal epithelial hyperplasia-like disease in a common chimpanzee
(Pan troglodytes) colony
                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; unclassified Papillomaviruses; Common chimpanzee papillomavirus.

1. (bases 1 to 7889)
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Scinicariello, F., Soza, I., Brasky, K.M. and Hilliard, J.K.
Direct Submission
Submitted (26-AUG-1997) Yerkes Primate Research Center, Emory
University, 954 Gatewood Dr NE, Atlanta, GA 30322, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Common chimpanzee papillomavirus 1"
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                                                     AF020905 7889 bp DNA linear V
Common chimpanzee papillomavirus 1, complete genome.
                                                                                                                                                                                Common chimpanzee papillomavirus 1
Common chimpanzee papillomavirus 1
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2728. .3858
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101. .559
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RESULT 6
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KDLFGVGFNDLVRQFKSDKSTCTDWVYSVFGVNPSIAEGFHMLLKEQTLYLHTQWVTC
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                                                                                                                             circular VRL 31-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSKYCVRHTCRPKPVAAHLTFFVVISNNYYACTKGSNRKRSDRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burk, R.D. and Terai, M. Direct Submission Direct Submission Submitted (14-SEP-2001) Microbiology & Immunology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, New York, NY 10461, USA
                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 7966)

Terai, M. and Burk, R.D.
Identification and Characterization of 3 Novel Genital Human Papillomaviruses by Overlapping Polymerase Chain Reaction: candHPV89, candHPV90, and candHPV91

J. Infect. Dis. 185 (12), 1794-1797 (2002)
                                                                                                                                                                                                                                   Human papillomavirus - cand91 (candHPV91)
Human papillomavirus - cand91
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 91, complete genome.
AF419318
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CDS

FEATURES

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YRFLANKAIACQKNVPPKAKEDPYKNYTFWDVDLTERFSAQLTQFPLGRKFVWQAGLR /translation="metlarrldmcQeQLLELYEKDSRDLQDHVLHWKCIRYECALYY KAREMGIKHLGHQVVPKLEVSRAKAHVAIEMQLSLESLLQTEYSIEPWTLQDTCQELW HTEPKKCFKKRGQTVEVRFDCNPENTMQYTLMSEIYVPVNDTWVKVHGHVDYKGLSYT /translation="MYLIPTPMCLHCLTQQXLLTLQSHLQQYLIYIHKQDLILHFLQC HLVSPMCHCHRLLHLLQYQYMAQIFIYILHCCILANAVNVFHIFLQITMWRLNDNKVY LPPPGPIASIVSTDEYVQRTNLFYHAGSSRLLAVGHPFFPIKNNSGKVIVPKVSGHQY /note="putative minor capsid protein L2" codon start=1 /product="L2" /note="putative major capsid protein Ll" /codon\_start=1 E2

ORIGIN

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SOURCE

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/db_xref="UniProt/TremBi.Q705H6"
/translation="MGKLDNGTLLMAQTSYILLHLYLVPSVKYPLLRLINLTPDQRPP
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QQVNLQVYRVVTECTSCLCVIRLVVQCSDSDIKKLEDLLLGTLKIVCPLCTTTAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMGANKGCGRGSSSVAEAVEVVEEAGATNSSQDIGEPSPRTRIIELFKDKDVTVKLLG
KFKELFGVGFNDLVRQFRSDKSTCTDWVYSVFGVNPSISBGFHMLLKEHTLYLHTQWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGNGSEVTGTTPEWISRQTMLEHSFADTQFSLTDMVQWAYDNGYTEEYDIAYYYAQRG
DIDANAAAFLKSNMQARYVRDCACMCKHYKLAEMKKMSWAEWIKHRGGKCNDGDWKPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKFLKYQHIDIIAPIGALKKWLHGIPKKNCICIIGPPDTGKSCFGMSLMKFLGGTILS
YVNASSHFWLQPLVDAKVAMLDDVTAGCWTYMDMHMRNLLDGNPTSIDRKHRALTVIK
CPPLLLTSNLDISTEDKYKYLRSRITTFFPNTFPFDTNGNAIYELNDENWNSFFKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCGQKHYYVEFHKEARTYGETGQWNVVMGSNVIYSPASVSSTVSEVSSVASTESDTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTVPDSTCTQKADCQGQAPPKKVRFDPHTTPIADLARTVGRGSVDSSDSRLVPKHT
DHHPRGHNRGSHTTPIIQLQGBANALKCFRYRLNKHKHLFADVSSTWRWTTECNNKTN
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THLNPAFTDPTIVQPTPPVEAGGRIIISHSTVTADSAEQIPMDTFVIHSDPTTSTPIP
GTAPRPRLGLYSKALQQVEIVDPTFLSSPQRLITYDNPVFEDPNATLTFEQPTVHEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESVDRDLSPRLHAIKIGGGQKAKRRLFHVTEQRDSTNGNTEVEARETQVEVEYGGPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FCRWGMVLLALCRYKVAKNRSTIVRQLAQMLNVPVQQILIQPPKLQSAPAALFWFRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tränslation="metlarrldmcoeqllelyekosktledhylhwkyiryecalyy
karragikhlghoyvpqleysrokayiaielomsleallotessepwtlodtsoevw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTEPOKCFKKRGOTVEVRYDCNPANAMHYTLWSDIYVPLNSTWLKVSGHVDYEGLSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MADKQGTEDEGLGCSGWFIVEATVDKTTENNISEDEIEDEEEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKWASMGVYFGGLGIGTGSGTGGRTGYVPLTTGRTGIVPKVTAEPGVVSRPPIVVES
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                                                                                                                                                                                                                                                                                                                                   'db_xref="GOA:Q705H8"
'db_xref="InterPro:IPR001177"
'db_xref="UniProt/TrEMBL:Q705H8"
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'db_xref="InterPro:IPR001866"
'db_xref="UniProt/TrEMBL:Q705H7"
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product="L2 protein"
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/db_xref="Gl:40804477"
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/db_xref="G1:40804478"
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'db_xref="GOA:Q705H5"
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product="E2 p
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/gene="E2"
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/gene="L2"
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/gene="E2"
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gene="E4"
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/gene="El"
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Human papillomavirus type 43 complete genome.
AJ620205
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Submitted (02-JAN-2004) de Villiers E.M., Div. Characterization of
Tumorviruses, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld
242, Heidelberg, 69120, GERWANY
Location/Qualifiers
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                                                                                                                                                                   Gaps
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Cloning and sequencing of the full-length genome of HPV 43
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ620205.1 GI:40804474
El gene; E2 gene; E4 gene; E6 gene; E7 gene; L1 gene; L2
gene; Y gene
Human papillomavirus type 43
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                                                                     Length 7966;
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/db.xref="G1:40804476"
/db_xref="GOA:Q705H9"
/db_xref="InterPro:IPR000148"
/db_xref="UniProt/TrEMBE:Q705H9"
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| specific host="Homo sapiens"
| db_xref="taxon:10591"
| 02. .569
   PRPKLKSGKRAAPSSSSAPASKRKKTKR"
                                                                                                 Score 27.4; DB Pred. No. 0.76; 0; Mismatches
                                                                                                                                                                                                                                                                                                    6453 GATGGTGATATGGTAGATACAGGGTTTGG 6481
                                                                                                                                                                                                                                         1 GATGGTGATATGGTAGATACAGGATTTGG 29
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protein id="CAF05783.1"
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                                                                                                 Query Match
Best Local Similarity . 96.6%;
Matches 28; Conservative
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de Villiers, E.M.
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/gene="E6"
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/gene="E7"
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/gene="E7"
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KEYWORDS
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man Williams

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Assert L. J. Sorma, S. R., Marshall, R. L. and Rahler, T. G. Short-chain nuclectide sequence of human papilloma virus patent: JP 2001231587-A 53 28-AUG-2001; ABBORATORIES OS Unidentified PR 2001231587-A/53 PD 28-AUG-2001; PP 31-JAN-2001 JP 2001231587-A/53 PD 28-AUG-2001 PP 31-JAN-2001 JP 200123187-A/53 PD 28-SEP-1990 US 590253 PR 28-SEP-1990 US 590253 PR 28-SEP-1990 US 590253 PI JEFPREY L JOSEPH, STANLEY R BORMA, RONALD L MARSHALL, THOWAS G PI RAHLER PC C12N15/00, C12M15/00, C12M
                                                                                                                                                                                                                                                                                                     PAT 03-APR-1996
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Bouma.S.R., Joseph.J.L., Marshall,R.L. and Laffler,T.G.
Bouma.S.R., Joseph.J.L., Marshall,R.L. and Laffler,T.G.
Mucleotide sequences useful as type specific probes, PCR priand LCR probes for the amplification and detection of human papilloma virus, and related kits and methods
Datent: US 5484699.A 53 16-JAN-1996;
Location/Qualifiers
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Short-chain nucleotide sequence of human papilloma virus.
BD017550
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                                                     6339 GATGGTGACATGGTAGATACAGGATTTGG 6367
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/organism="unknown"
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Sequence 53 from patent US 5484699.
117042
117042.1 GI:1251950
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        1 GATGGTGATATGGTAGATACAGGATTTGG
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JP 2001231587-A/53.
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/db_xref="GI:40804483"
/db_xref="UniProt/TrEMBL:Q705H2"
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/framslation="MGIVCPFFYAGNKCSLDIFLIKLVKLATLCLPICILLALIPGPK,
/A86. .7854
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/product="protein Lla"
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/brocein id="CaPo5790.1"
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ATVPDIYAQTGPDISFPTIPIHIPYIPVSPSISPQSVSIHGTDFYLHPSLMHLGKRRK
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//FATBFGRVWHPYSWCDHUGRLLCFCQNMLAHFLSLWRQGVASYAHIPLLLYKCTFS
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protein id="CAF05792.1"
db_xref="G1:40804484"
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5673. .7268
/gene="L1"
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/gene="X"
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/gene="Y"
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/gene="L1"
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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the virus and reagent for
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CI2N15/09, A61K38/00, A61K39/12, A61K39/395, A61K39/395, A61K48/00,
A61P31/20,
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2 (Lur, B.M.D.V., Hausen, H.Z., Lavergne, D. and Benton, C.

Papilloma virus, reagent for detecting the virus and reagent for

treating diseases caused by the virus

Patent: JP 2001505767-A 2 08-MAY-2001;

DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES EFFENTLICHEN RECHTS

PN JP 2001505767-A/2
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12-MOV-1997 JP 1998524126
26-MOV-1996 DE 19648962.8
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Mammalia, Euthéria, Euarchontoglires, Primates, Catarrhini,
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De Villiers-Zur Hausen, E.-M., Zur Hausen, H.,
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                            Score 25.8; DB 6;
Pred. No. 4.8;
0; Mismatches 2;
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Pred. No. 4.8;
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Sequence 6 from patent US 6413522.
AR216809
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/mol_type="genomic DNA"
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JP 2001505767-A/2.
Homo sapiens (human)
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Best Local Similarity 93.1
Matches 27; Conservative
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/db_xref="G1:6740701"
/tb_xref="G1:6740701"
/tb_xref="G1:674070
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Zur, H.H. and Lavergne, D.

PAPILLOMA VIRUSES, AGENTS FOR DETECTING THE SAME AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES

Patent: WO 9823752-A 2 04-JUN-1998;

DEUTSCHES KREBSFORSCH (DE); ZUR HAUSEN HARALD (DE)

Location/Qualifiers
                                                   Gaps
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De Villiers-Zur Hausen, E.-M., Zur Hausen, H., Lavergne, D. and
Benton, C.
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Score 25.8; DB 6; Length 38;
Pred. No. 6.1;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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AR216808.1 GI:23316083
                                                                                              1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Sequence 2 from Patent WO9823752.
A91822
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/wol_type="genomic DNA"
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unidentified
unclassified sequences.
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Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative
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Matches 27; Conservative
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

RESULT 12 AR216808

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Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Unclassified Papillomaviridae.

I (Dases 1 to 386)
de Villiers, E.M., Lavergne, D., McLaren, K. and Benton, E.C.
Prevaling papillomavirus types in non-melanoma carcinomas of the skin in renal allograft recipients
Int. J. Cancer 73 (3), 356-361 (1997)
 C07K14/025, C07K16/08, C12N1/19, C12N1/21, C12N5/10, C12Q1/68, PC
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (28-MAY-1997) de Villiers E.M., Deutsches
Krebsforschungszentrum, Tumorvirus Charakterisierung 0660, Im
Neuenheimer Feld 242, 69120, Heidelberg, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .386
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="isolated from Skin squamous cell carcinoma biopsy, WV-9021; partial HPV L1 seque"
/specific host="Homo sapiens"
/db_xref="taxon:10566"
/clone lib="DL20"
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Human papillomavirus DNA for partial HPV L1 sequence.
295953
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89.0%; Score 25.8; DB 6; Length 386;
Best Local Similarity 93.1%; Pred. No. 4.8;
Matches 27; Conservative 0; Mismatches 2; Indels
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    .386
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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                                                                                                                                 Location/Qualifiers
PC C07K14/025,C07K16/08,C1
C12N15/00,
PC C17N5/00,A61K37/02
CC C17N5/00,A61K37/02
CC Topology: Linear;
CC Topology: Linear;
CC /desc = 'DNA' LOCATIO
FH Key 1.384
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de Villiers, E.M.
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Best Local Similarity 93.14
Matches 27; Conservative
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HPVZ95953
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nucleic search, using sw model OM nucleic -

5, 2006, 21:50:08; Search time 380.5 Seconds (without alignments) 507.953 Million cell updates/sec March Run on:

US-10-720-424B-1 Title: Perfect score:

gatggtgatatggtagatacaggatttgg 29 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4996997 segs, 3332346308 residues Searched:

9993994 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

N\_Geneseq\_21:\*

geneseqn2003cs:\* geneseqn2001bs: geneseqn2003as:\* geneseqn2003bs: geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\* geneseqn2002as: geneseqn2002bs: geneseqn2001as:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:\*

geneseqn2004as

geneseqn2005s:\* geneseqn2004bs:

### SUMMARIES

		de				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	29	100.0	29	12	ADQ27974	Adq27974 Human pap
8	25.8	89.0	38	7	AA023183	Aag23183 HPV probe
٣	25.8	89.0	38	7	AAT29878	Aat29878 Human pap
4	25.8	89.0	386	7	AAV15595	Aav15595 Papilloma
Ŋ	25.8	89.0	1421	ω.	AAL47486	Aal47486 HPV type
9	. 25.8	89.0	1497	14	AEA12674	Aea12674 DNA encod
7	25.8	89.0	1524	7	AAT40119	Aat40119 Human pap
80	25.8	89.0	1950	7	AAQ04472	Aaq04472 Human pap
6	25.8	89.0	2017	н	AAN91804	Aan91804 Human pap
10	25.8	89.0	7824	14	ADZ45651	Adz45651 Human pap
11	25.8	89.0	7857	14	ADZ45648	Adz45648 Human pap
12	25.8	89.0	7880	12	ADN12113	Adn12113 HPV type
13	25.8	89.0	7896	12	ADN12111	Adn12111 HPV type
14	24.2	83.4	410	7	AAT47256	Aat47256 (DSM 1009
15	24.2	83.4	1422	12	ADF89368	Adf89368 Plant-opt
16	24.2	83.4	1443	12	ADF89363	Adf89363 Plant-opt
17	24.2	83.4	1452	10	ACC47503	Acc47503 HPV 16 L1
18	24.2	83.4	1452	10	ACC47505	Acc47505 HPV 16 L1
1	24.2	83 4	1494	~	AADO1237	Aad01237 Chimeric

Add01238 Chimeric Adf89361 Plant-opt Ad816246 Human pap Ad816247 Human pap Aav7167 HPV1 L1 O Aav09856 HPV16 rec Aav25817 Human pap Aav12161 Human pap Aav12161 Human pap Aav12161 Human pap Aav12161 Human pap Aav240564 HPV16 L1 Ad62855 Human pap Adc26169 HPV16 L1 Ad62855 Human pap Aav37566 Human pap	AD158976 HPV16-L1 Abx11395 Hwman pap Abx11395 Hwman pap Ada27368 HPV-16 L1 Ada27368 HPV-16 L1 Ada14295 HPV-16 L1 Ada14295 HPV-16 L1 Ad47895 HPV-16 L1 Ac47502 HPV-16 L1 Ac47504 HPV 16 L1 Ac47504 HPV 16 L1 Ac47504 HPV 16 L1 Ac47504 HPV 16 L1 Adf83436 Human pap Adf83440 Human pap
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3 AAD01238 12 ADF89361 13 ADS16246 13 ADS16247 2 AAV09856 2 AAV125817 2 AAV125817 2 AAV125817 2 AAV125112 3 AAZ40564 10 ADC26169 12 ADG2855 2 AAX3566	AMD
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0 10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	,

## ALIGNMENTS

Human papillomavirus genotype detection PCR primer #4. ss; primer; detection; diagnosis; amplification; Human Papillomavirus genotype; cervical-neoplasia; oncogenic high-risk group. BB ADO27974 standard; DNA; 29 (first entry) 09-SEP-2004 AD027974; RESULT 1 ADQ2797 

Human papillomavirus. WO2004050917-A1.

17-JUN-2004.

28-NOV-2003; 2003WO-KR002608.

29-NOV-2002; 2002KR-00075370. 31-JUL-2003; 2003KR-00053147.

(ALBI-) ALBIOMED CO LTD.

Ko J; Cha K, Yu K, Kim S, Lee S, Kim Y,

WPI; 2004-450746/42.

New general primer or primer pair, useful for amplifying and detecting, or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV genotypes.

Claim 1; SEQ ID NO 4; 71pp; English.

The invention relates to a general primer or primer pair for amplifying and detecting or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes. The general primers are useful for amplifying cervical-neoplasia related HPV genotypes including

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oncogenic high-risk groups and low-risk groups. The general primers are useful for producing amplifying products to DNA of scores of diverse oncogenic HPV types and thus detecting the oncogenic HPV types in a sample but also to select cervical carcinoma and its pre-stage lesions at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specificity of prior-art antibody based tests. The oligonucleotides can be used either to detect specific sequences of specific HPV types, or consensus regions with homology among different types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compsns. for amplifying DNA of human papilloma virus by LCR and PCR - consensus and type specific oligo-nucleotide(s), for diagnosis of HPV-esp. types 6,11,16,18 33 and 61.
                                                                                                                                                                                                              Gaps
                                                                          early stage by improving sensitivity according to HPV types. This sequence corresponds to PCR primer used in the invention.
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                                                                                                                                                                     ; Score 29; DB 12; Length 29; Pred. No. 0.0099; 0; Mismatches 0; Indels
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                                                                                                                                   Sequence 29 BP; 8 A; 1 C; 11 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                   1 GATGGTGATATGGTAGATACAGGATTTGG 29
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                                                                                                                                                                       100.0%;
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90US-00590105.
90US-00590253.
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                                                                                                                                                   July Match
Best Local Similarity 100...
Conservative
                                                                                                                                                                                                                                                                                                                                                                                   AAQ23183 standard; DNA; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-1992 · (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-106365/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
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The sequences AAT29826-T29921 represent primers and probes derived from human papillomvirus genomic sequences and are used to detect the presence of human papillomavirus types 6, 11, 16, 18, 31 and 33 in samples. The detection is either by PCR or LCR. Alternatively the sequences can be labelled with fluorescein or biotin and used as probes. (Updated on 25-
                                                                                                                                                                   primer; probe; human papillomvirus; PCR; amplification; LCR; ligation;
fluorescein; biotin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          the detection of and determination of the type of HPV in test
                                                                                                                                                                                                                                                                                                                                                                                                                                               New human papilloma virus type-specific oligo:nucleotide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 89.0%; Score 25.8; DB 2; Length 38; 1 Similarity 93.1%; Pred. No. 0.25; 27; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papillomavirus major capsid protein DNA from plasmid DL20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38 BP; 8 A; 3 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                Joseph JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                              Human papillomavirus detection probe 36.
 1 GATGGTGATATGGTTGATACAGGCTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                Laffler TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Col 13-14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                          90US-00589948.
90US-00590105.
90US-00590253.
92US-00965665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAR-2003 to correct PF field.)
                                                              ВР
                                                                                                                                                                                                                                                                                    94US-00316293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV15595 standard; DNA; 386
                                                              AAT29878 standard; DNA; 38
                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Bouma SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-087060/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                        28-SEP-1990;
28-SEP-1990;
22-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                 Marshall RL,
                                                                                                                                                                                                                                                                                    30-SEP-1994;
                                                                                                             25-MAR-2003
19-JUL-1996
                                                                                                                                                                                                                                     US5484699-A.
                                                                                                                                                                                                                                                            16-JAN-1996
                                                                                                                                                                                                                                                                                                             28-SEP-1990;
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30-JUL-1998
                                                                                                                                                                                                              Synthetic.
                                                                                      AAT29878;
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AAV15595
                                      RESULT 3
                                                   AAT29878
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Gaps

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The present invention relates to a composition for preventing or treating tumours caused by human papillomavirus (HPV) 18, involving at least one fusion protein of at least one each of L and E proteins from one or more papillomaviruses, and optionally also additives or auxiliaries. The composition can be used as a vaccine to treat or prevent carcinoma of the lung, cervix, penis, vulva and anus. The present sequence is an HPV gene
                                                                                                                                                                                                                           Composition for treating and preventing tumors caused by human papilloma virus 18, contains fusion protein of papilloma virus L and E proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      papillomavirus infection; uterine cervix tumor; carcinoma; HPV58 L1; virus-like particle; vaccine; expression; recombinant protein; transformation; immune stimulation; virucide; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding human papillomavirus 58 L1 protein, 58 L1 wt sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 1421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1421. BP; 371 A; 260 C; 316 G; 474 T; 0 U; 0 Other;
                                                                                                                                  Gabelsberger J, Herbst R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25.8; D
Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             589 GATGGTGATATGGTAGATACTGGATATGG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                                                                                                                                                                                      Disclosure; Page 14-15; 64pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "HPV58 L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                        01-DEC-2000; 2000DE-01059630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEA12674 standard; DNA; 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.0%;
Best Local Similarity '93.1%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                preferably truncated.
                                                                                                                                  Nieland
                                                                                                                                                                      WPI; 2002-520969/56
                                                                                             (MEDI-) MEDIGENE AG
                                                                                                                                                                                          P-PSDB; AA018098.
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                                                                                                                                Mueller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEA12674;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes a fragment of the human papillomavirus (PV) major capsid protein isolated from plasmid DL20. This fragment could be used as a reagent for detecting PV infections and diseases (e.g. warts or cancers of skin, cervix or mouth/throat, particularly of the skin). Cells containing transformants can be used to produce recombinant papillomavirus which can be used for diagnosis, treatment and prevention (as vaccines) of papillomavirus infection. (Updated on 25-MAR-2003 to
   skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 18; HPV; cancer; L protein; E protein; cytostatic; virucide; vaccine; lung; cervix; penis; vulva; anus; gene;
Major capsid protein; detection; infection; disease; wart; cancer; sk diagnosis; treatment; prevention; vaccine; cervix; mouth; throat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding peptide(s) from papilloma virus major capsid protein - a related proteins, vectors, transformed cells and antibodies, for diagnosis, treatment and prevention of papilloma virus infection and
                                                                                                                                                                                                                                                                                                                                                                                                Zur Hausen H, Lavergne D, Benton C;
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                                                                                       5;
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                                                                                                                                                                                                                                                                                                                                                           (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL47486 standard; DNA; 1421 BP
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                                                                                                                                                                                                                                                                               96DE-01048962
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Best Local Similarity 93.1%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            De Villiers- Zur Hausen E,
                                                        Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-121621/12.
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                                                                                                                                                                                                       DE19648962-C1
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New nucleic acid molecule encoding HPV58 L1, useful for immunoprophylaxis

WPI; 2005-372343/38. P-PSDB; AEA12673.

DE10059630-A1

Synthetic.

AAL47486;

RESULT 5

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06-JUN-2002

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Gaps

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papillomavirus (HPV) infection. More than 90% of cervical carcinomas are associated with infections of HPV31, HPV-33, -45, -52, and -58. The L1 associated with infections of HPV31, HPV-33, -45, -52, and -58. The L1 confidence is the major capsid protein and is highly conserved among different papillomaviruses. Expression of the L1 and L2 proteins in capsile of inducing high titres of neutralizing antibodies when administered into animals, without the potentially oncogenic viral administered into animals, without the potentially oncogenic viral cargets for the development of prophylactic and therapeutic vaccines for HPV infection. Vaccine development has been identified as immunological cargets for the development of prophylactic and therapeutic vaccines for HPV infection. Vaccine development has been limited by difficulties in obtaining high expression levels of capsid proteins. The present contains a nucleic acid (SEQ ID NO: 1) encoding HPVSB is protein (SEQ ID NO: 2), which is codon-optimized for high-level expression in yeast cells. Virus-like particles (VLDR) are also disclosed comprised of recombinant L1 protein or recombinant L1 + L2 proteins of HPVSB L1 gene, and cultivating the yeast under conditions that permit che HPVSB L1 gene, and cultivating the yeast under conditions that permit che WPVSP The The gene and vaccine are useful for immunoprophylaxis against containing the passion of the VDEs The gene and vaccine are useful for immunoprophylaxis against containing the passion of the VDEs The gene and vaccine are useful for immunoprophylaxis against containing the passion of the VDEs The gene and vaccine are useful for immunoprophylaxis against containing the passion of the VDEs The gene and vaccine are useful for immunoprophylaxis against containing the vaccine comprising containing the passion of the VDES L1 gene are useful for immunoprophylaxis against containing the passion of containing the passi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        papillomavirus infection, and for treating existing human papillomavirus infection. The present sequence is DNA encoding human papillomavirus 58 L1 protein, designated 58 L1 wt.
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serotyping; cervix carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
against papillomavirus infection, and for treating existing human
                                                                                                                          new invention relates to the prevention and therapy of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4;
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                                                                          Disclosure; SEQ ID NO 3; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
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95US-00409122.
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Best Local Similarity 93.1
Matches 27; Conservative
                            papillomavirus infection.
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P-PSDB; AAW05843.
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22-MAR-1995;
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DNA encoding human papilloma virus 18, esp. L1 and L2 capsid proteins

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papilloma-virus type 52 DNA and RNA - used in probes for detecting HPV infection in samples and for blocking HPV gene expression.
                                                                                    The L1 gene (AAT40119) codes for the major capsid protein (AAW05843) of human papillomavirus type 18 (HPV18), an HPV type associated with invasive carcinomas of the cervix, vagina, vulva and anal canal. The DNA sequence was deduced from a genomic clone isolated from human cervical carcinoma-derived SW756 cells using an HPV18 L1 probe. The HPV18 L1 and L2 (see also AAT40120) genes can be used in vaccines against HPV18 infection, as probes, or to produce recombinant capsid proteins in host
and related vectors and antibodies, useful in protective vaccines, for serotyping HPV infections and as therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papilloma virus type 52; HPV infection; probes; cervical cancer;
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                        Length 1524;
                                                                                                                                                                                                                                                  Sequence 1524 BP; 396 A; 292 C; 337 G; 499 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papilloma virus 52 clone pCD15 noncoding region.
                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                        0.4;
                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       GATGGTGATATGGTAGATACTGGATATGG 617
                                                                                                                                                                                                                                                                                                                                                             GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                                                                                                                                                                        Score 25.8;
                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                        Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88US-00262597.
                                                        Claim 2; Fig 1; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89EP-00310934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ04472 standard; DNA; 1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 52
                                                                                                                                                                                                                                                                                                       1 Similarity 93.1%;
27; Conservative
                                                                                                                                                                                                                                                                                          89.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lancaster WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP370625-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ04472;
                                                                                                                                                                                                                                                                                                                                                                                                589
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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Z, Lusk J;

Wang

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RESULT 9 AAN91804

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New composition having a nucleic acid molecule identical to genomic clone of human papilloma virus 16, 18 or 51, useful in diagnosing cancer or the risk of developing cancer, in particular cervical, anal, colon and HPV-related cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of developing cancer, in particular cervical, anal, colon and HPV-related cancer. The present DNA sequence represents a human papilloma virus full length genomic clone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises a composition for the detection of cancer markers, the composition contains a nucleic acid molecule which is substantially identical to a full length genomic clone of a human papilloma virus (type 11, 16, 18, 51, 56, 58, 66, 70, or 73). The composition of the invention is useful for diagnosing cancer or the
Human papillomavirus type 58 full length genomic clone - SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7824 BP; 2487 A; 1388 C; 1576 G; 2373 T; 0 U; 0 Other;
                             genome; diagnosis; cancer; uterine cervix tumor; colon tumor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14; Length 7824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome; diagnosis; cancer; uterine cervix tumor; colon tumor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type 18 full length genomic clone
                                                                                                                                                                                                                                                                                                               Rasmussen OF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6231 GATGGTGACATGGTAGATACAGGGTTTGG 6259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match
Local Similarity 93.1%; Pred. No. 0.90.188 27; Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                                                                                                                                                                                               Bisgaard-Franzen K, Lin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 5; 169pp; English.
                                                                                                                                                                                                                                                                                (DAKO-) DAKOCYTOMATION DENMARK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                             07-OCT-2003; 2003DK-00001474.
07-OCT-2003; 2003US-0509205P.
13-FEB-2004; 2004US-0543925P.
                                                                                Human papillomavirus type 58.
                                                                                                                                                                               04-OCT-2004; 2004WO-DK000670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 7857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2004; 2004WO-DK000670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-2003; 2003DK-00001474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                Yoast S;
                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-285441/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADZ45648 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2005033333-A2.
                                                                                                                 WO2005033333-A2
                                  marker;
                                                   rectal tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rectal tumor;
                                                                                                                                                                                                                                                                                                                                Lindberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2005
                                                                                                                                                 14-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADZ45648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                 Chau MF,
                                    tumor
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ADZ45648
ID ADZ45
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Used as a probe. The patent describes probes (DNA or RNA) and their complements capable of detecting one or a combination of HPV types 6, 16, 18, 31, 33 and 35. (Updated on 25-WAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rapid detection of specific human papilloma virus genotypes - by hybridisation of DNA digest with new labelled nucleic acid probes.
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                                                                 Score 25.8; DB 2; Length 1950;
Pred. No. 0.42;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2017 BP; 583 A; 399 C; 373 G; 662 T; 0 U; 0 Other;
                                  Sequence 1950 BP; 551 A; 376 C; 380 G; 643 T; 0 U; 0 Other;
 field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                  Human papilloma virus type 33 marker fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGGTGATATGGTAGATACAGGATTTGG 29
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                                                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89WO-US001318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-00177404
89US-00330381
                                                                 Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative
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Best Local Similarity 93.1.
Best Local 27; Conservative
                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Groff DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1989-324314/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ONCO-) ONCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     Cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-1988;
31-MAR-1989;
                                                                                                                                                                                                                                                                                                                                25-MAR-2003
16-MAR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          George AL,
                                                                                                                                                                                                                                                                                AAN91804;
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- SEQ ID 2.

RESULT 10

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ADZ45651

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Example 1; SEQ ID NO 6; 218pp; English.
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                                                                                                                                                                                                                                                                                                                    6321
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 8 X C C C C C C C C C X S
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                          New composition having a nucleic acid molecule identical to genomic clone of human papilloma virus 16, 18 or 51, useful in diagnosing cancer or the risk of developing cancer, in particular cervical, anal, colon and HPV-
                                                                                                                                                                                                                                                                                                                 of developing cancer, in particular cervical, anal, colon and HPV-related cancer. The present DNA sequence represents a human papilloma virus full length genomic clone of the invention.
                                                                                                                                                                                                                                                            markers, the composition contains a nucleic acid molecule which is substantially identical to a full length genomic clone of a human papilloma virus (type 11, 16, 18, 51, 56, 58, 66, 70, or 73). The composition of the invention is useful for diagnosing cancer or the risk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    major histocompatibility class I; MHC-I; MHC-II; Cytostatic; BBV-associated cancer; Hodgkin's lymphoma; nasopharyngeal carcinoma; gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma; parotid carcinoma; breast carcinoma; leiomvosarcoma; As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human cell line modified to comprise and express genes encoding immunomodulators and an antigen of Epstein-Barr virus (EBV), useful for inducing or stimulating an immune response in a human to EBV-associated
                                                                       Lusk J;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                The invention comprises a composition for the detection of cancer
                                                                                                                                                                                                                                                                                                                                                                           Sequence 7857 BP; 2365 A; 1497 C; 1680 G; 2315 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 7857;
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                                                                       Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                       Rasmussen OF,
                                                                                                                                                                                                                                                                                                                                                                                                      DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levitsky HI;
                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6201 GATGGTGATATGGTAGATACTGGATATGG 6229
                                                                                                                                                                                                                                                                                                                                                                                                     Match
Local Similarity 93.1%; Pred. No. 0.5;
es 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                      Lin J,
                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrello IM,
                                           (DAKO-) DAKOCYTOMATION DENMARK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN12113 standard; DNA; 7880 BP
                                                                      Bisgaard-Franzen K,
1, Yoast S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2003; 2003WO-US029684
 07-OCT-2003; 2003US-0509205P
13-FEB-2004; 2004US-0543925P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPV type 13 genome #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Papilloma Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ambinder RF, Yang Y,
                                                                                                                 WPI; 2005-285441/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-295406/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004027036-A2.
                                                                                                                                                                                        cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VINU ( OCYU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN12113;
                                                                                      Lindberg
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                       Chau MF,
                                                                                                                                                                                        related
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Matches
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cancer.

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The present invention relates to a human cell line, which lacks major histocompatibility class I (MHC-I) and MHC-II antigens and which has been modified to comprise and express a gene encoding an immunomodulator and a gene encoding an antigen of Epstein-Barr virus (EBV). The human cell line, compositions and methods are useful for inducing or stimulating an immune response in a human to an EBV-associated cancer, where the human has or is at risk for Hodgkin's lymphoma, T-cell lymphoma, B-cell lymphoma, parctic carcinoma, Burkitt's lymphoma, T-cell lymphoma, B-cell lymphoma, sequence represents a nucleotide sequence associated with the cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a human cell line, which lacks major histocompatibility class I(MHC-I) and MHC-II antigens and which has been modified to comprise and express a gene encoding an immunomodulator and a gene encoding an antigen of Epstein-Barr virus (EBV). The human cell line, compositions and methods are useful for inducing or stimulating an immune response in a human to an EBV-associated cancer, where the human has or is at risk for Hodgkin's lymphoma, nasopharyageal carcinoma, gastric carcinoma, burkitt's lymphoma, T-cell lymphoma, B-cell lymphoma, parotid carcinoma, breast carcinoma, and leiomyosarcoma. The present sequence represents a nucleotide sequence associated with the cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 major histocompatibility class I; MHC-I; MHC-II; Cytostatic; EBV-associated cancer; Hodgkin's lymphoma; nasopharyngeal carcinoma; gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma; parotid carcinoma; breast carcinoma; leiomyosarcoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human cell line modified to comprise and express genes encoding immunomodulators and an antigen of Epstein Barr virus (EBV), useful for inducing or stimulating an immune response in a human to EBV-associated cancer.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                           Sequence 7880 BP; 2452 A; 1480 C; 1628 G; 2320 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                       Length 7880;
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                                                                                                                                                                                                                                                                                                                       DB 12;
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                                                                                                                                                                                                                                                                                                                                                 0.5;
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                                                                                                                                                                                                          Score 25.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 4; 218pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2003; 2003WO-US029684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN12111 standard; DNA; 7896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-2002; 2002US-0411990P.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Papilloma Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-295406/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome
                                                                                                                                                                                                                                      the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004027036-A2
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(first entry)

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papillomavirus virus-like particle, capsomere, transgenic, plant,
L1 capsid, gene therapy, HPV16, ds, gene, mutant.
                                                                                     Plant-optimised NLS-deleted Human papillomavirus type 16 Ll DNA.
 ADF89368 standard; DNA; 1422 BP.
                                                                                                                                                                          Human papillomavirus type 16.
                                                           26-PEB-2004
                                                                                                                                                             Synthetic
                              ADF89368;
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence, which encodes a human papillomavirus (HPV) major capsid (L1) protein, is 69.4% homologous to the HPV48 L1 DNA. The encoding DNA, which is contained in pV2201-1 (DSM 10097), is useful for the diagnosis of HPV disease, especially skin cancer, and for the preparation of the protein. The protein is useful for the diagnosis,
                                                                                                                                                                                                                                                                                                                                      major; capsid; L1; HPV48; pVS201-1; DSM 10097; diagnosis; disease; cancer; therapy; prevention; vaccination; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding peptide(s) of papilloma major capsid protein - useful for diagnosis, treatment and prevention of papilloma virus disease.
                                                                                        Gaps
                            Sequence 7896 BP; 2473 A; 1457 C; 1594 G; 2372 T; 0 U; 0 Other;
                                                                                      ö
                                                           Length 7896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24.2; DB 2; Length 410;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                           (DSM 10097) human papillomavirus major capsid protein DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preparation of the protein. The protein is useful for the therapy and prevention (by vaccination) of these diseases
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 410 BP; 116 A; 69 C; 99 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zur Hausen H;
                                                         12;
                                                                                     7
                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                          1. 408
/*tag= a
/label= major_capsid_protein
                                                                                                                                     6194 GATGGTGATATGGTAGACACAGGATATGG 6222
                                                                                     0; Mismatches
                                                                                                                 1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                         Score 25.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Villiers-Zur Hausen E,
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 3; 15pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95DE-01026386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95DE-01026386
                                                        Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 83.4%;
1 Similarity 89.7%;
26; Conservative
                                                                                                                                                                                                                    AAT47256 standard; DNA; 410
                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043923/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW07854.
of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE19526386-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shamanin V,
                                                                                                                                                                                                                                                                              05-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JAN-1997
                                                                                                                                                                                                                                                AAT47256;
                                                                                                                                                                                                                                                                                                                                                       skin
                                                                                                                                                                                         RESULT 14
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8XCCCCCCCX8X44X44X44X4X4X4X4X444444X8XX4X4X4X8X

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The invention relates to a novel method for producing papillomavirus virus-like particles or capsomeres comprising providing a transgenic plant or plant seed transformed with a nucleic acid molecule comprising papillomavirus il capsid protein coling sequences and growing the transgenic plant or transgenic plant grown from the transgenic plant seed under conditions effective to produce the virus-like particles containing the papillomavirus il capsid protein. The invention may have virucide applications whilst the methods, genetic construct and plant may be unseful for immunising a subject against a disease resulting from infection by a papillomavirus, as well as during gene therapy procedures. The current sequence is that of the plant-optimised NLS (nuclear localisation signal)-deleted Human papillomavirus type 16 (HPV16) L1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing papillomavirus virus-like particles or capsomeres comprises providing a transgenic plant or plant seed transformed with a nucleic acid molecule comprising a papillomavirus L1 capsid protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1422;
                                                             /*tag= a
/product= "Plant-optimised NLS-deleted Human
papillomavirus type 16 L1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1422 BP; 384 A; 343 C; 296 G; 399 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24.2; DB Pred. No. 1.9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   589 GATGGTGATATGGTGGATACTGGCTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5, 2006, 22:12:07
Location/Qualifiers
1. .1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Warzecha H;
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                                                                                                                                                                                                                                                                                                       02-MAY-2003; 2003WO-US013757
                                                                                                                                                                                                                                                                                                                                                           02-MAY-2002; 2002US-0377467P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.4%;
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Best Local Similarity 89.7
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rose RC, Mason HS,
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Job time : 383.5 secs
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P-PSDB; ADF89369.
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Gaps

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Indels

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0; Mismatches

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1 GATGGTGATATGGTAGATACAGGATTTGG

GATGGTGATATGGGTGATATAGGATTTGG 41

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ઠ 셤 RESULT 15 ADF89368

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QBM4a04.x n129a01.8 HS\_3023\_B HS\_5009\_B CITBI-EI-tigr-988-StrPu691.

QBM2b09.x

602273477 N001G08.3 UI-CF-DU1 hggfha39D 601562994

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CW750547 OP Ba006
CC087160 GR Ea05H
BQ223384 AGENCOURT
AK042726 Mus muscu
(EB13095 tigr-988-
DR532869 WS02739.C
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This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 bp mRNA linear EST 08-APR-2002 BB170020B10F08.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170020B10F08 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apidae; Apis.

T (bases 1 to 601)

Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.
Anocated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apis mellifera (honey bee)
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DU075702 80192 Ton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="mixed strains of Buropean bees, predominantly
A.m. ligustica"
/db.xef="ksxxx:7460"
/clone="BB170020B10F08"
                                          A1609976
CF017655
CF017813
AA578113
AQ334764
AQ334764
AQ35473
AQ357438
CE148431
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Contract: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: ATTAACCCTCACTAAAG
Plate: BB170020B10 row: F column: 08
Seq primer: AGCGATAACAATTCACACAGA
High quality sequence stop: 601.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l. .601
'organism="Apis mellifera"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                          AAS78113
AQ093787
AQ337438
CE148431
CD307313
BF970237
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DR532869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIS05309
BIS05309.1 GI:15355683
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                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
BI505309
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CW611284 OA AB8015
AG537642 Mus muscu
CZ694085 OCC B8000
AL836861 AL836817
AL124517 Fugu rubr
BJ14819 Fugu rubr
BR277163 601178502
AI020455 ub26605.r
AA210582 mur1803.r
BR547434 u831g01.x
BX513029 BX513029
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Z39966 HSC1NH042 n
CV376112 PM3-SN001
AW207569 UI-H-BI1-
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AZ693668 AST-2HLB5
AW273632 xv67h03.x
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                                                                                                                                                   5, 2006, 21:59:29 ; Search time 3168 Seconds (without alignments) 428.291 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                       41078325 seqs, 23393541228 residues
                                                                                                                                                                                                                                                                                          gatggtgatatggtagatacaggatttgg 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum Match O%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL836861
AZ159603
FR0037014
                                                                                                          nucleic search, using sw model
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AG537642
CZ694085
AL836877
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AA210582
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                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB seq length: 0
DB seq length: 200000000
                                                                                                                                                                                                                                        US-10-720-424B-1
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Match Length DB
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9b est2: *
9b est2: *
9b est4: *
9b est4: *
9b est5: *
9b est7: *
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9b est7: *
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Result Š

Post-processing:

Minimum | Maximum |

Database

Perfect score:

Title:

Seguence:

OM nucleic

Run on:

Scoring table:

Searched:

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B 2074s28.

E 2 (Dases 1 to 738)

S Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

B Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Direct Submission.

Lored Submission.

Lored Submission.

1-7-22 Sub
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                                                                                                                                                                                         AG537642 73-DEC-2004 NA linear GSS 23-DEC-2004 Mus musculus molossinus DNA, clone:MSMg01-449L22.T7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contribution of Asian mouse subspecies Mus musculus molossinus to espendic constitution of strain C57BL/63, as defined by BAC-end sequence-SNP analysis Genome Res. 14 (12), 2439-2447 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
Shiroishi,T.
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/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus molossinus (Japanese wild mouse)
Mus musculus molossinus
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350 GATGGAGATATGGTAGAAAAGAGGATGAGG 378
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/sub_species="molossinus"
/db_xref="taxon:57486"
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Matches 24; Conserve
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                         /tissue type="brain"
/dev stage="adult worker honey bee"
/lab/host="Bullt worker honey bee"
/lab/host="Bullt Bullton"
/clone lib="Bee Brain Normalized/Subtracted Library, BB17"
/clone lib="Bee Brain, Vector: pT713-Pac; Site_1: EcoR;
/note="Organ: brain; Vector: pT773-Pac; Site_1: EcoR;
Site_2: Not1; This BB17 cDNA library was generated by subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806 RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups."
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Oryza australiensis
Oryza australiensis
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 687)
Kim, H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ontact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
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/lab_hogt="DH10B T1 phage resistant"
/clome_lib="OA_ABa"
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/mol_type="genomic DNA"
/db_xref="taxon:4532"
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Email: biohelp@hgmp.
Email: biohelp@hgmp.
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/mol type="genomic DNA"
/db xref="taxon:77588"
/db xref="taxon:77588"
/foot="tasue type="tasues"
/dev stage="mature"
/dev stage="mature"
/doo ilb="nog Ba"
/clone lib="nog Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Erhartoideae; Oryzeae; Oryza.

1 (bases 1 to 810)

Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
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(lark, M. S., Edwards, Y. J., Peterson, D., Clifton, S.W., Thompson, A.J., Susaki, M., Suzuki, Y., Kikuchi, K., Watabe, S., Kawakami, K., Suzuki, X., Kakuchi, K., Watabe, S., Kawakami, K., Fugu ESTs: new resources for transcription analysis and genome
                                                                                                                                                                                                               Wing, R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
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Contract: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Fal: 520 621 1259
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Contact: Clark MS
MRC Human Genome Mapping Project Resource Centre
Hinxton, Cambridge, CB10 1SB, UK
                                                     Oryza coarctata (Porteresia coarctata)
Oryza coarctata
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/mol type="qenomic DNA"
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BACKWARD: CAC TCA TTA GGC ACC CCA
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Class: BAC ends.
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Takifugu rubripes
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CZ694085.1 GI:71093233
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                                                                                                                                                                                                                                       The clone can be obtained from www.hgmp.mrc.ac.uk
Library created by Greg Elgar
RC Human Genome Mapping Project Resource Centre, Hinxton,
Cambridge, CBIO 1.5B. UK
Library sequenced by Sarah Warner and Jim Hills
MRC Human Genome Mapping Project Resource Centre, Hinxton,
Cambridge, CBIO 1.5B. UK.
Location/Qualifiers
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Library created by Greg Elgar
MRC Human Genome Mapping Project Resource Centre, Hinxton,
Cambridge, CB10 1SB. UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript II KS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.0%; Score 20.6; DB 1; illarity 85.2%; Pred. No. 4.5e+02; Conservative 0; Mismatches 4;
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/mol_type="mRNA"
/db_xref="taxon:31033"
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Takifugu rubripes
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/db_xref="taxon:31033"
/clone="BFRe040apcK8"
biohelp@hgmp.mrc.ac.uk
biohelp@hgmp.mrc.ac.uk
pBluescript II KS
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/clone_lib="EFRe"
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PRIMER: KS
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ORIGIN

RESULT 7 AZ159603/c LOCUS

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ORGANISM

ACCESSION

VERSION KEYWORDS

REFERENCE AUTHORS

PUBMED JOURNAL

COMMENT

TITLE

FEATURES

ORIGIN

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Generation and analysis of 25 Mb of genomic DNA from the pufferfish Pugu rubripes by sequence scanning Genome Res. 9 (10), 960-971 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ148396 unpublished oligo-capped cDNA library, C. elegans Ll stage Caenorhabditis elegans cDNA clone ykl262d04 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elgar, G. Clark, M.S., Smith, S., Meek, S., Warner, S., Edwards, Y.J.K., Umrania, Y., Williams, G. and Brenner, S.

Direct Submission
Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email:

Diohelp@Appm.mrc.ac.uk
Vector: pBluescript II KS
                                                                                                                                                                                             Actinopterygii, Neopterygii, Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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Kohara; Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                           Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.J., Bouchireb, N., Cottage, A., Yeo, G.S., Umrania, Y., Williams, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One pass dye-terminator sequencing of cosmid cloned genomic sequence.
Fugu rubripes GSS sequence, clone 045108bB5, genomic survey
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A complementary view of the C elegans genome Unpublished (2002)
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/organism="Takifugu rubripes"
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/clone="045108bbs"
/clone_lib="cosmid 045108"
                                                                                             GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
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Caenorhabditis elegans
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ALĪ24517.1 GI:6106132
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Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Bukaryota; Metazoa; Echinodemata; Eleutherozoa; Echinozoa;
Butaryota; Bucchinoidea; Echinodea; Echinoida;
Strongylocentrotidae; Strongylocentrotus;
Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
Mray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H.
and Hood,L.
Assa urchin genome project: Sequence scan, virtual map, and
                                                                                                                                                                                                                                                                                                                                                                                                                                         SP_0064_A2_E10_T7A Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=64 Col=20 Row=I, genomic survey sequence.
AZI59603.1 GI:8312225
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10920195
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                                                                                                                                             71.0%; Score 20.6; DB 1; Length 370; 85.2%; Pred. No. 4.5e+02; ative 0; Mismatches 4; Indels
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|mol_type="genomic DNA"
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Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
                      /tissue type="gonad"
/clone_lib="EFRe"
/note="Vector: pBluescript II KS"
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High quality sequence stop: 465.
Location/Qualifiers
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  /clone="EFRe040apcKl'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus
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Plate: 64 row: I column: 20
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                                                                                                                                             Query Match
Best Local Similarity
Matches 23; Conserv
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Best Local Simi
Matches 23;
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RESULT 8 FR0037014 LOCUS

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Dubuque, T.,

us-10-720-424b-1.rst

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//clone lib="soares_thymus_2NbMT"
//clone lib="soares_thymus_site"
//clone lib="soares_thymus_site"
//clone lib="soares_thymus_site"
//clone lib=stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTTT3 vector. RNA
//clone lib=strand Jordan. Library went through two
                                                                                                                                                                  AI020455 250 bp mRNA linear EST 16-JUN-1998 ub26g05.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1378904 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        provided by Dr. Bertrand Jordan. Library went through rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 250)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: MarshU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.3%; Score 20.4; DB 1; Length 250; 95.5%; Pred. No. 5.2e+02; ive 0; Mismatches 1; Indels
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                                                            529 recrerrracracacacacarrres 555
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                      59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 234
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:1378904"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Thymus"
/dev_stage="4_weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="mRNA"
strain="CS7BL/6J"
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Seq primer:
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                                                                                                                                                                                           DEFINITION
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Place: LLCOR7 row: d column: 01
                                                                                                                                                                                                             /dev stage="11"
/clone lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Concact: Robert Strausberg, Ph.D.
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Thsuse Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                         Length 770;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                            /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                         Score 20.6; DB 3;
Pred. No. 4.9e+02;
                                                                                                                                              /clone="yk1262d04"
/sex="hermaphrodite"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             558 ATGGGGATATGGTAGACAAAGGACTTG 532
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/db_xref="taxon:9606"
/clone="IMAGE:3050832"
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Location/Qualifiers
                                                                                                                                db xref="taxon:6239"
Email: tshini@genes.nig.ac.jp.
                      Location/Qualifiers
                                                                                 /mol_type="mRNA"
/strain="N2"
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                                                                                                                                                                                                                                                                                                                            71.0%;
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1 (bases 1 to 776)
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Best Local Similarity 85.2
Matches 23; Conservative
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Best Local Similarity
Matches 23; Conserv
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TITLE
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Euteleostomi;

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BX513029 Soares mouse lymph node NbWLN Mus musculus cDNA clone IMAGE:644812, mRNA sequence.
                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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Mus musculus
Musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (Dases 1 to 528)
Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D. and Korn,B.
                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi, Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 490)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.3%; Score 20.4; DB 2;
95.5%; Pred. No. 5.7e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Mus musculus"
                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 474. Location/Qualifiers
1. .490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:10090"
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                  Mus musculus (house mouse)
Mus musculus
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Unpublished (2003)
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BX513029.1 GI:32244756
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/dev_stage="4 weeks"
/dab_host="4 weeks"
/lab_host="Togan: Union of the libe"Soares mouse lymph node NbMLN"
/note="Crgan: lymph node; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
[5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Patima Bonaldo."
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             AA210582 327 bp mRNA linear EST 29-JAN-1997 mu71a03.rl Soares mouse lymph node NbMLN Mus musculus cDNA clone IMAGE:644812 5', mRNA sequence.
                                                                                                                                                                                                                                                      1 (bases 1 to 327)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geigel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Mooze,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Nakaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse BST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forrest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 5.4e+02;
0; Mismatches 1;
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/mol type="mRNA"
strain=C57BL/6"
/db xref="taxon:10090"
/clone="IMAGE:644812"
                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
The WashU-HHMI Mouse EST Project
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                                                                                                                                                    Mus musculus (house mouse)
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                                                                                                         AA210582.1 GI:1807829
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1 Similarity 95.5%;
21; Conservative (
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BF147434
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Best Local Similarity
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                    LOCUS
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ORGANISM
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AA210582/c
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BF147434
                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
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                                                                                  ACCESSION
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Gaps

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Length 490; 1; Indels

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Search completed: March 5, 2006, 23:57:58 Job time: 3173 secs
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                           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Soares mouse lymph node NbMLN" hote="Organ: Lymph node; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; lst strand cDNA was primed with a Not I - oligo (dI) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www.rzyd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
T7, Primer seguence: TAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                    RZPD; IMAGD952J0565.

RZPDI.B; I.M.A.G.E. CDNA Clone Collection;
Mouse Unigeneset - RZPDZ (RZPDLIB No.981)

http://www.rzpd.de/cloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=981 Contact: Ina Rolfs
bin/showLib.pl.cgi/response?libNo=981 Contact
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101

Pax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.3%; Score 20.4; DB 5; Length 528;. Best Local Similarity 95.5%; Pred. No. 5.7e+02; Matches 21; Conservative 0; Mismatches 1; Indels 0
     Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGp952J0565 ; IMAGE:644812"
Im Neuenheimer Feld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mashington University School of Medicine
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Insert Length: 175000 Std Brror: 0.00
Seq primer: RM1 TACGACTCACTATAGGGAGA
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="male"
                                                                                                                                                                                                                                                                                                                                                                      source
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CL056918/c
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/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                       Length 1020;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                     Score 20.2; DB 10;
Pred. No. 7.6e+02;
0; Mismatches 3;
                                                    /organism="Xenopus tropicalis"
                                                                     /mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-83P3"
High quality sequence stop: 551.
                                                                                                                                                                                                                                                                                                                                                                                  844 regrentregradarangekirr 820
                                                                                                                                                                                                                                                                                                                                               3 TGGTGATATGGTAGATACAGGATTT 27
                  Location/Qualifiers
                                                                                                                                                                                                                                                                   ch 69.7%;
1 Similarity 88.0%;
22; Conservative
                                                                                                                                                 /sex="male"
                                 1, .1020
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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March 5, 2006, 19:08:04; Search time 80.5 Seconds (without alignments) 640.364 Million cell updates/sec
GenCore version 5.1.7
• Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2606114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*/cgn2_6/ptodata/1/ina/PP_COMB.seq:*/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/ina/backfiles1.seg:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents NA:*

1. /cgn2 6/pcdata/l/ina/l_COMB.seq:*

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4. /cgn2 6/ptodata/l/ina/6A_COMB.seq:*

4. /cgn2 6/ptodata/l/ina/6B_COMB.seq:*

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6. /cgn2 6/ptodata/l/ina/R_COMB.seq:*

6. /cgn2 6/ptodata/l/ina/R_COMB.seq:*
                                                                                                                                                                                                                                                                                            1 gatggtgatatggtagatacaggatttgg 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                      1303057 segs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                   US-10-720-424B-1
29
                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		ф				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	25.8	89.0	38	~	US-08-316-293-53	Sequence 53, Appl
7	25.8	89.0	386	ო	US-09-319-056B-4	4,
. c	25.8	89.0	386	e	US-09-319-056B-6	6
4	25.8	89.0	1524	~	US-08-409-122-1	٦,
S	25.8	89.0	1524	~	US-08-408-669-1	Sequence 1, Appli
9	25.8	89.0	1524	ო	US-08-913-644-1	ı,
7	24.2	83.4	410	ო	US-09-000-266-7	Sequence 7, Appli
ω υ	24.2	83.4	410	ო	US-09-000-266-9	Sequence 9, Appli
6	24.2	83.4	410	m	US-09-628-099-7	7
c 10	24.2	83.4	410	m	US-09-628-099-9	6
11	24.2	83.4	410	m	US-10-056-360-7	Sequence 7, Appli
c 12	24.2	83.4	410	ო	US-10-056-360-9	6
13	24.2	.83.4	410	ო	US-10-056-359-7	7
c 14	24.2	83.4	410	m	US-10-056-359-9	6
15	24.2	83.4	1494	ო	US-09-413-611A-5	Sequence 5, Appli
16	24.2	83.4	1500	m	US-09-413-611A-7	7,
17	24.2	83.4	1517	N	US-08-032-869A-2	Sequence 2, Appli
18	24.2	83.4	1517	N	US-08-472-673-2	Sequence 2, Appli
19		83.4	1517	~	US-08-475-782-2	'n
20		83.4	1517	N	US-08-472-678-2	7
21	24.2	83.4	1517	N	US-08-484-503-2	Sequence 2, Appli
22	24.2	83.4	1518	٣	US-08-944-368A-1	٦,
23	24.2	83.4	1518	٣	US-09-820-764-1	г Т
24	24.2	83.4	1518	m	US-09-986-118A-1	Sequence 1, Appli

בה הה הה הה הה היה היה היה היה היה היה ה	Sequence 1, Appli Sequence 8, Appli
US-09-824-017-1 US-08-710-082-5 US-08-710-082-20 US-08-913-462-5 US-08-913-462-5 US-09-624-482-5 US-09-624-482-20 US-08-578-634-20 US-08-578-634-20 US-08-578-634-20 US-08-578-634-2 US-08-578-634-2 US-08-578-634-2 US-08-578-634-2 US-08-578-634-2 US-08-578-634-2 US-08-578-634-2 US-08-578-634-2 US-08-77-2-67-11 US-08-77-78-11 US-08-472-678-1	US-08-484-503-1 US-08-815-667-8
	7 7
1518 125 125 125 125 125 125 661 662 663 668 668 668 1484 1517 1517	1517 1518
8	77.9
4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	22.6 22.6
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44 45

## ALIGNMENTS

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US-08-316-293-53
US-08-316-293-53
US-08-316-293-53
PAREL INFORMATION:
APPLICANT: ABBOTT LABORATORIES
APPLICANT: Thomas G. Laffler
TITLE OF INVENTION: PAPLICANCTORES; PCR PRIMERS AND LCR PROBES
TITLE OF INVENTION: POR THE AMPLIFICATION AND DETECTION OF HUMAN
TITLE OF INVENTION: PAPLICANCES; 96
CORRESPONDENCE ADDRESS;
ADDRESSE: Abbott Laboracories
STREET: One Abbott Park Road
CITY: Abbott Park Road
COUNTRY: USA
STREET: ONE Abbott Park Road
COUNTRY: USA
COUNTRY: USA
TILING DATE: NOTGEFIECE 5.0
COMPUTES: IN PC COMPATION: ABSISTANCE CASSIFCATION DATA:
APPLICATION NUMBER: US/09/365,665
FILING DATE:
TREETOM COUNTRY: USA
APPLICATION NUMBER: US/07/965,665
FILING DATE:
TREETOM COUNTRY: USA
TREETOM COUNTRY: USA
APPLICATION NUMBER: US/07/965,665
FILING DATE:
TREEDOMMUCATION NUMBER: 12,483
REGISTRATION NUMBER: 13,483
REGISTRATION NUMBER: (708) 337-484
TELECOMMUCATION NUMBER: (708) 37-484
TELECOMMUCATION NUMBER: (708) 37-484
TELECOMMUCATION NUMBER: (708) 37-484
TELECOMMUCATION NUMBER: (708) 37-484
TELECOMUCATION NUMBER: (708) 37-484
TELECOMMUCATION NUMBER:
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Gaps

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Indels

Length 386;

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APPLICANT: JOYCE, JAMES G.
APPLICANT: GEORGE, HUGH A.
APPLICANT: GEORGE, HUGH A.
APPLICANT: HOFMANN, KATHRYN J.
APPLICANT: JANGEN, KATHRYN J.
APPLICANT: NEEPER, MICHAEL P.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLLOMAVIRUS TYPE 18 VACCINE NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CRRISTINE E. CARTY - MERCK & CO., INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000 CITY: RAHWAY
                                                                                            Score 25.8; DB 3;
Pred. No. 0.15;
                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                             380 GATGGTGATATGGTAGACATAGGATTTGG 352
                                                                                                                                                                                            1 GATGGTGATATGGTAGATACAGGATTTGG
                                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-409-122-1
Sequence 1, Application US/08409122
; Patent No. 5820870
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-6734
                                                                                          Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 93.1
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 908-594-67.
TELEFAX: 908-594-4720
                       Papilloma virus
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ORIGINAL SOURCE:
US-08-409-122-1
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                    , ORGANISM: Pa
US-09-319-056B-6
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APPLICANT: Denton, Claire
TITLE OF INVENTION: PAPILLOMA VIRUSES, PRODUCTS FOR THE
TITLE OF INVENTION: PAPILLOMA VIRUSES, PRODUCTS FOR TREATING DISEASES CAUSED BY
TITLE OF INVENTION: THEM
FILE REPRENCE: 8444-0086-99
CURRENT APPLICATION NUMBER: US/09/319,056B
CURRENT FILING DATE: 1997-01-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
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APPLICANT: bonna
APPLICANT: benton, Claire
TITLE OF INVENTION: PAPILLOMA VIRUSES, PRODUCTS FOR THE
TITLE OF INVENTION: DETECTION THEREOF AS WELL AS FOR TREATING DISEASES CAUSED BY
TITLE OF INVENTION: THEM
FILE REFERENCE: 8484-0086-999
CURRENT PAPLICATION NUMBER: 1099-08-05
PRIOR PAPLICATION NUMBER: 1099-08-05
PRIOR APPLICATION NUMBER: DET/DE97/02659
PRIOR APPLICATION NUMBER: DE 196-08-05
PRIOR APPLICATION NUMBER: DE 196-11-26
PRIOR PILING DATE: 1996-11-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 386
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89.0%; Score 25.8; DB 3; Length 386;
Best Local Similarity 93.1%; Pred. No. 0.15;
Matches 27; Conservative 0; Mismatches 2; Indels
                                         Query Match
Best Local Similarity 93.1%; Pred. No. 0.12;
Matches 27; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                            1 GATGGTGATATGGTAGATACAGGATTTGG 29
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                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09319056B Patent No. 6413522 GENERAL INFORMATION:
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ORGANISM: Papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (1)...(384)
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US-08-316-293-53
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LENGTH: 386
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,122
FILLING DATE:
                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/408,669
FILING DATE: 22-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTIBE B
REGISTRATION NUMBER: 36,099
REFRENCE/DOCKET NUMBER: 19425
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Gaps

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GENERAL INFORMATION:

APPLICANT: Shamanin, Vladimir

APPLICANT: Shamanin, Vladimir

APPLICANT: Shamanin, Harald

APPLICANT: De Villiers-Zur Hausen, Ethel-Michele

APPLICANT: THE ABBLICANT: ALT HARALING BERNES FOR DETECTING

TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES;

TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES;

TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES;

TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES;

CURRENT APPLICATION NUMBER: PCT/DE96/01369

EARLIER FILING DATE: 1996-10-19

EARLIER FILING DATE: 1996-07-19

SARLIER FILING DATE: 1995-07-19

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 7

LENGTH: 410
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APPLICANT: Shamanin, Vladimir
APPLICANT: Shamanin, Vladimir
APPLICANT: De Villiere-Zur Hausen, Ethel-Michele
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: PAPLICANA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
FILE REFERENCE: 8484-0037-999
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89.0%; Score 25.8; DB 3;
Best Local Similarity 93.1%; Pred. No. 0.18;
Matches 27; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: HPV18 L1 Consensus Sequence US-08-913-644-1
PRIOR APPLICATION NUMBER: PCT/US96/03649
PRIOR FILING DATE: 1996-03-18
PRIOR PILING DATE: 1995-03-22
PRIOR FILING DATE: 1995-03-22
PRIOR PILING DATE: 1995-03-22
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 1
SEQ ID NO 1
LENTH: 1524
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                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Papilloma virus
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; LOCATION: (1)...(408)
US-09-000-266-7
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US-09-000-266-9/c
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                                                                                                                                                        APPLICANT: HOFMANN, KATHRIN J.
APPLICANT: JANSEN, KATHRIN U.
APPLICANT: NEEPER, MICHAEL P.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1524;
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APPLICANT: Jansen, Kathrin U.
APPLICANT: Neeper, Michael P.
APPLICANT: Neeper, Michael P.
APPLICE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE
TITLE OF INVENTION: 18
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                                                                                                                                                                                                                                                                                                            ADDRESSEE: CHRISTINE B. CARTY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STARE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,669
FILING DATE: 22-MAR-1995
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Patent No. 6908615
GENERAL INFORMATION:
                                                                               Sequence 1, Application US/08408669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CARTY, CHRISTINE E
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 93.1%;
Matches 27; Conservative
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FILE REFERENCE: 19424PC
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; ORIGINAL SOURCE:
US-08-408-669-1
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**Gaps** 

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RESULT 12
US-10-056-360-9/c
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US-10-056-360-7
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APPLICANT: Shamanin, Vladimir
APPLICANT: Shamanin, Vladimir
APPLICANT: Shamanin, Vladimir
APPLICANT: Sure Hausen, Harald
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES;
FILE REFERENCE: 8484-0037-999
CURRENT APPLICATION NUMBER: US/09/628,099
CURRENT FILING DATE: 1998-10-19
PRIOR APPLICATION NUMBER: DE P 195 26 386.3
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SSEQ ID NO 7
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Patent No. 636832
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shamanin, Vladimir
APPLICANT: De Villiers-Zur Hausen, Ethel-Michele
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: PAPILLOWA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
FILE REFERENCE: 8484-0037-999
CURRENT APPLICATION NUMBER: US/09/628,099
CURRENT FILING DATE: 2000-05-26
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Pred. No. 0.71;
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89.7%; Pred. No. 0.71;
ive 0; Mismatches 3; Indels
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CURRENT APPLICATION NUMBER: US/09/000,266A
CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: PCT/DE96/01369
EARLIER FILING DATE: 1996-07-19
EARLIER APPLICATION NUMBER: DE P 195 26 386.3
EARLIER FILING DATE: 1995-07-19
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 410
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09628099
Patent No. 6368832
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
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Best Local Similarity 89.7
Matches 26; Conservative
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TYPE: DNA
ORGANISM: Papilloma virus
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; LOCATION: (1)...(408)
US-09-628-099-7
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US-09-628-099-7
                                                                                                                                                                                                                              TYPE: DNA
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Shamanin, Vladimir

APPLICANT: Shamanin, Vladimir

APPLICANT: Cur Hausen, Harald

APPLICANT: Cur Hausen, Harald

TITLE OF INVENTION: PAPPLILOMA VIRUSES, AGENTS FOR DETECTING

TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES

FILE REFERENCE: 8464-0037-999

CURRENT PILING DATE: 2000-01-23

CURRENT PILING DATE: 2000-01-23

FRIOR PRILING DATE: 1996-10-19

FRIOR PILING DATE: 1998-10-19

FRIOR PILING DATE: 1998-10-19

FRIOR FILING DATE: 1998-10-19

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FRASEQ for Windows Version 3.0
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APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: PAPILLAMA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
FILE REFERENCE: 8484-0037-999
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                                                                                                                                                                                                                                                                                                                                                                                                                              398 GATGGTGATATCGGTGATATAGGATTTGG 370
PRIOR APPLICATION NUMBER: 09/000,266
PRIOR FILING DATE: 1998-10-19
PRIOR APPLICATION NUMBER: DE P 195 26 386.3
PRIOR FILING DATE: 1995-07-19
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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Pred. No. 0.
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Pred. No. 0.
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; Patent No. 6555345
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.1 Similarity 89.7%;
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Best Local Similarity 89.7°
Matches 26; Conservative
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CORGANISM: Papilloma virus
US-09-628-099-9
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Best Local Similarity
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Search completed: March
Job time : 81.5 secs
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APPLICANT: Shamanin, Vladimir
APPLICANT: Shamanin, Vladimir
APPLICANT: Shamanin, Vladimir
APPLICANT: Sur Hausen, Harsald
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES;
FILE REFERENCE: 8484-0037-999
CURRENT APPLICATION NUMBER: US/10/656,359
CURRENT APPLICATION NUMBER: US/09/628,099
PRIOR PILING DATE: 2001-05-08
PRIOR PILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
SPRIOR FILING DATE: 1998-07-19
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FABLESQ for Windows Version 3.0
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APPLICANT: Shamanin, Vladimir
APPLICANT: Shamanin, Vladimir
APPLICANT: De Villiers-Zur Hausen, Ethel-Michele
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
FILE REFERENCE: 8484-0037-999
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Pred. No. 0.71;
0; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: US/09/628,099
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/000,266
PRIOR PILLING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
PRIOR APPLICATION NUMBER: DE P 195 26 386.3
PRIOR FILING DATE: 1995-07-19
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 410
                                                                                                                                                                                                                                                                                                                                                     Score 24.2; DE . Pred. No. 0.71; 0; Mismatches
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Patent No. 6562597
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Patent No. 6562597
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Best Local Similarity 89.7%;
Matches 26; Conservative
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Best Local Similarity 89.7
Matches 26; Conservative
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ORGANISM: Papilloma virus
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ORGANISM: Papilloma virus
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; LOCATION: (1)...(408)
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Nieland, John
Velders, Markwin
VBNTION: Chimeric Biotin-Binding Papillomavirus Protein
NCE: 202325
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PRIOR APPLICATION NUMBER: US/09/628,099
PRIOR FILING DATE: 2001-05-09
PRIOR PELING DATE: 1090-109
PRIOR PILING DATE: 1998-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1995-07-19
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTERO FOR Windows Version 3.0
SEO ID NO 9
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                                                                                                                                                                                                                                                                                                                       Score 24.2; DE Pred. No. 0.71; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Patent No. 6380364
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Best Local Similarity 89.7%;
Matches 26; Conservative
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US-10-056-359-9
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; LOCATION: (1)..(1491)
US-09-413-611A-5
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                                                                                                                                                                                                              LENGTH: 410
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| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US099_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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(c) 1993 - 2006
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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APPLICANT: Lee, Sang-Wha
APPLICANT: Kim, Yeon-Soo
APPLICANT: Kim, Yeon-Soo
APPLICANT: Kim, Seung-Vool
APPLICANT: Kim, Seung-Vool
APPLICANT: Kim, Seung-Vool
APPLICANT: Kim, Seung-Vool
APPLICANT: Ko, Jung-Jae
TITLE OF INVENTION: HUWAN PAPLICLOMAVIRUS BY PCR
TITLE OF INVENTION: HUWAN PAPLICANTON WHORER: US/10/720,424B
TITLE OF INVENTION NUMBER: KR10-2002-0075370
PRIOR PELING DATE: 2002-11-29
PRIOR PELING DATE: 2003-01-11-29
PRIOR FILING DATE: 2003-01-31
PRIOR FILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 16
SOOFWARE: Patentin version 3.2
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US-09-864-408A-8573

US-10-475-203A-7

US-09-970-477-2

US-10-475-203A-3

US-10-371-846-1

US-10-371-846-1

US-10-367-095-12

US-10-367-095-12

US-10-368-046-12

US-10-368-046-12

US-10-368-046-12

US-10-368-087-12

US-10-918-337-12

US-10-918-337-12

US-10-12-178-1

US-10-056-359-28

US-10-056-359-28

US-10-056-359-28

US-10-056-359-22

US-10-056-359-22

US-10-056-360-22

US-10-056-360-24

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Publication No. US20040248085A1
GENERAL INFORMATION:
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Publication No. US20040101533A1
GENERAL INFORMATION:
APPLICANT: MULLER, RAINER
APPLICANT: NIELAND, JOHN
APPLICANT: GABELSBERGER, JOSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-1
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APPLICANT: Lee, Sang-Wha
APPLICANT: Kim, Yeon-Soo
APPLICANT: Yu, Kang-Yeol
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Matches 29; Conservative
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LENGTH: 410
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                                                                                                                                                                                                                 SEQ ID NO 9
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APPLICANT: HERBST, RUTH
TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS TYPE 18
FILE REPERENCE: 037067/0115
CURRENT APPLICATION NUMBER: US/10/433,091
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PLING DATE: 2001-12-01
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 1
LENGTH: 1421
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                          Query Match 89.0%; Score 25.8; DB 7; Length 1421; Best Local Similarity 93.1%; Pred. No. 1.2; Matches 27; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
83.4%; Score 24.2; DB 5; Length 410;
Best Local Similarity 89.7%; Pred. No. 4.4;
Matches 26; Conservative 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                 589 GATGGTGATATGGTAGATACTGGATATGG 617
                                                                                                                                                                                                                                                                                                                                       1 GATGGTGATATGGTAGATACAGGATTTGG 29
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                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Human papillomavirus type 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...(408)
US-10-056-359-7
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US-10-056-359-9/c
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                                                                                                                                                                                                                                               US-10-433-091-1
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Sequence 9, Application US/10056359; Publication No. US20020110865A1; GENERAL INFORMATION: APPLICANT: Shamanin, Vladimir; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele

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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Shammain, Vladimir

APPLICANT: Car Hausen, Harald

TITLE OF INVENTION: PAPPLILLOMA VIRUSES, AGENTS FOR DETECTING

TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES

FILE REFERENCE: 8484-0037-99

CURRENT PILING DATE: 2000-01-23

FRIOR APPLICATION NUMBER: US/10/658,360

PRIOR APPLICATION NUMBER: 09/9000,266

PRIOR PILING DATE: 1998-10-19

PRIOR FILING DATE: 1998-10-19

PRIOR FILING DATE: 1998-07-19

NUMBER OF SEQ ID NOS: 30

SOFTWARRE FASEED (for Windows Version 3.0)

SOFTWARRE FASEED (for Windows Version 3.0)
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APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: PAPILICANA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
FILE REFERENCE: 8484-0037-999
CURRENT APPLICATION NUMBER: US/10/056,359
CURRENT FILING DATE: 2002-01-23
PRIOR FILING DATE: 2002-01-25-08
PRIOR PLICATION NUMBER: 09/000,266
PRIOR PLICATION NUMBER: 09/000,266
PRIOR APPLICATION NUMBER: 09/000,266
PRIOR PLILNG DATE: 1998-10-19
PRIOR APPLICATION NUMBER: DE P 195 26 386.3
PRIOR PLILNG DATE: 1995-07-19
PRIOR PLILNG DATE: 1995-07-19
PRIOR FILING DATE: 1995-07-19
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PRIOR FILING DATE: 1995-07-19
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Pred. No. 4.4;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998 GATGGTGATATGGGTGATATAGGATTTGG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 CATGGTGATATGGGTGATATAGGATTTGG 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)...(408)
US-10-056-360-7
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US-10-056-360-9/c
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SEQUENCE CHARACTERISTICS
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LENGTH: 1452
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APPLICANT: Tybicki, Edward
APPLICANT: Tybicki, Edward
APPLICANT: Williamson, Anna-Lise
TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and
TITLE OF INVENTION: Pharmaceutical Compositions for Prophylactic Treatment of
TITLE OF INVENTION: Desions and Carcinomas
TITLE OF INVENTION: Lessions and Carcinomas
TITLE OF INVENTION: Lessions and Carcinomas
TITLE OF INVENTION: Lessions and Carcinomas
TITLE OF INVENTION: LOSA55-116
CURRENT APPLICATION NUMBER: US/10/487,719
PRIOR APPLICATION NUMBER: 2004-02-27
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASTESEQ for Windows Version 4.0
            TITLE OF INVENTION: PAPILICAMA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
TITLE REFERENCE: 8484-0037-999
CURRENT FILING DATE: 2000-01-23
PRIOR APPLICATION NUMBER: US/09/628,099
PRIOR APPLICATION NUMBER: 09/000,266
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-07-19
NUMBER OF SEQ ID NOS: 30
SOFTWARE: RESELECT FOR WINDOWS VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
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De Villiers-Zur Hausen, Ethel-Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Pred. No. 4.
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US-10-487-719-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.4
Best Local Similarity 89.7
Matches 26; Conservative
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APPLICANT: Varsani, Arvind
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Papilloma virus
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Best Local Similarity
Matches 26; Conserv
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SEQ ID NO 9
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LENGTH: 1452
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US-10-487-719-4
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APPLICANT: Williamson, Anna-Lise
TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and
TITLE OF INVENTION: Isolating Said Pharmaceutical Compositions, and Use of Said
TITLE OF INVENTION: Desions and Carcinomas
TITLE OF INVENTION: Lesions and Carcinomas
CURRENT APPLICATION NUMBER: 105/10/487,719
PRIOR FILING DATE: 2004-02-27
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: ZA 2001/7228
PRIOR PELICATION NUMBER: ZA 2001/7228
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ADDRESSEE: KNOBEN. MARTENS, OLSON & BEAR
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/832,065
FILING DATE: 09-Apr-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/316,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPILLOMAVIRUS CAPSID PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24.2; D
Pred. No. 5.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 4
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 OTHER INFORMATION: fragment of L1 gene US-10-487-719-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kirkpatrick Ph.D., An REGISTRATION NUMBER: 32,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dilication No. ...
GENERAL INFORMATION:
APPLICANT: Lowy, Douglas R.
Schiller, John T.
Kirnbauer, Reinhard
Kirnbauer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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Publication No. US20030050439A1
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92660
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 89.79
Matches 26; Conservative
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DB 6; Length 1517;

Indels

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Score 24.2; D
Pred. No. 5.5;
                                                                                                            0, Mismatches
    SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                  83.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 28
                                                                                   Best Local Similarity 89.7
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-162-904A-1
        ;
US-10-371-846-2
                                                                                                                                                                                                                                                           RESULT 11
US-09-820-765-1
                                                                    Query Match
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                                                                                                                                                                                                                                                                               Query Match 83.4%; Score 24.2; DB 3; Length 1517; Best Local Similarity 89.7%; Pred. No. 5.5; Matches 26; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DESCRIPE: E105/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/371,846
FILING DATE: 21-Feb-2003
CIASSIFICATION: AUNROWN>
PRIOR APPLICATION OF THE COMPANION:
APPLICATION NUMBER: US/08/032,869
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: US 07/941,371
FILING DATE: 03-SEP-1992
ATTORNEY/AGENT INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lowy, Douglas R.
Schiller, John T.
Kirnbauer, Reinhard
TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
PAPILLOMAVIRUS CAPSID PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kirkpatrick Ph.D., Anita M.
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: NIH032.001CP1
                                                                                                                                                                                                                                                                                                                                                                                                    589 GATGGTGATATGGTTGATACTGGCTTTGG 617
                                                                                                                                                                                                                                                                                                                                                                   1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                                                                           LOCATION: 1..1517
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1517 base pairs
LENGTH: 1517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FRATURE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10371846 Publication No. US20030219873A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92660
                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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US-10-371-846-2
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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/820,765

FILING DATE: 30-Mar-2001

CLASSIFICATION: AUNKNOWN-

PRIOR APPLICATION: AUNKNOWN-

PRIOR APPLICATION NUMBER: US 09/026,896

FILING DATE: 20-FEB-1998

ATORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELEPHONE: (202) 672-5399

INFORMATION FOR SEQ ID No: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1518 base pairs
                                                                                                                                                                                                                 Sequence 1, Application US/09820765
; Publication No. US20020039584A1
; GENERAL INFORMATION:
    APPLICANT: BURGER, Alexander
; APPLICANT: BURGER, Michael
; TITLE OF INVENTION: PAPTILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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83.4%; Score 24.2; D
Best Local Similarity 89.7%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches
                                                                                             589 GATGGTGATATGGTTGATACTGGCTTTGG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 GATGGTGATATGGTTGATACTGGCTTTGG 617
                                                  1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
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; LOCATION: 1..1515
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-820-765-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATGGTGATATGGTAGATACAGGATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Gaps
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                                                                                                                                                                                              TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIAN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,017
PILING DATE: 03-Apr-2001
CLASSIFICATION 142
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                        FORMULATIONS AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock. Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.4%; Score 24.2;
89.7%; Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..1515
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09986118A
Publication No. US20030021806A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
                                                                                                             GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
                                                         Sequence 1, Application US/09824017
Publication No. US20020197668A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1518 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 89.7
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-986-118A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-017-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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; OTHER INFORMATION: HPV16 DNA clone P114/16/11
US-09-162-904A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of L1 ger
OTHER INFORMATION: HPV16 DNA clone P114/16/2
                                                                        APPLICANT: GISSMANN, LUCZ
TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
TITLE OF INVENTION: B 4844-068-999
FILE REFERENCE: 8484-068-999
CURRENT APPLICATION NUMBER: US/09/162,904A
CURRENT FILING DATE: 1998-09-29
PRIOR PILING DATE: 1997-06-27
PRIOR PILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/902,528
PRIOR PILING DATE: 1993-07-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Durst, watthias
APPLICANT: Durst, watthias
APPLICANT: Durst, watthias
APPLICANT: Gissmann, lutz
TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLCOMAVIRUS L1 PROTEIN CAPABLE
TITLE OF INVENTION: OF EFFICIENTLY FORMING VIRUS-LIKE PARTICLES
FILE REFERENCE: 8484-068-999 (209162,904A
CURRENT PAPLICATION NUMBER: 1998-09-29
PRIOR PILING DATE: 1997-06-27
PRIOR PILING DATE: 1997-06-27
PRIOR PLING DATE: 1996-05-01
PRIOR FILING DATE: 1996-05-01
PRIOR PLING DATE: 1996-05-01
PRIOR PLING DATE: 1996-05-01
PRIOR FILING DATE: 1096-05-01
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89.7%; Pred. No. 5.5;
ive 0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              589 GATGGTGATATGGTTGATACTGGCTTTGG 617
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Patent No. US20020168372A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1993-07-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 89.7
Matches 26; Conservative
                                                   APPLICANT: Durst, Matthias
US20020168372A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 1518
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COMPTRY: U.S.A.

ZIP: 2007-1218:
ZIP: 20007-1218:
ZIP: 20007-1218:
ZIP: 20007-1218:
ZIP: 20007-1218:
ZORDUTER: IND PC compatible
COMPUTER: IND PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: 07-NO. US20030021806A1-2001
CLASSIFICATION NUMBER: US 09/026,896
FILING DATE: cURKNOWN-
ATTORNAY/AGENT INFORMATION:
ATTORNAY/AGENT INFORMATION:
ATTORNAY/AGENT INFORMATION:
TELEPHONE: (202) 672-5300
TELEPHONE: (202) 672-5300
TELEPHONE: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: DNA (genomic)
FEATURE:
NAME/EXECUE TYPE: DNA (genomic)
FEATURE:
NAME/EXECUED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.4%; Score 24.2; DB 3; Length 1518; Best Local Similarity 89.7%; Pred. No. 5.5; Matches 26; Conservative 0; Mismatches 3; Indels 0;
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; LOCATION: 1..1515

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-986-118A-1
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Search completed: March 5, 2006, 22:49:27 Job time : 362 secs

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us-10-720-424b-1.rnpbn

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Sequence 8739, Ap
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Sequence 717454,
Sequence 575086,
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Sequence 1, Appli
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Sequence 484856,
Sequence 13230, A
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Sequence 18, App
                                                                                                                          March 5, 2006, 22:06:14 ; Search time 457 Seconds
(without alignments)
139.129 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 8, A
Sequence 10,
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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ptodata/1/pubpna/US10_NEW_PUB.seq:
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US-09-925-065A-484856
US-10-995-561-13230
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US-09-925-065A-883719
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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No.
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Seguence 821943,	Sequence 561682,	Sequence 561683,	. Sequence 111263,	Sequence 899601,	Sequence 899602,	Sequence 233861,	Seguence 233862,	Sequence 3498, Ap	Sequence 652774;	Seguence 1855, Ap	Seguence 5497, Ap	Sequence 1855, Ap	Seguence 5497, Ap	Sequence 875490,	Seguence 34733, A	Sequence 713292,	Sequence 25879, A	Sequence 25879, A	38674,	Sequence 38674, A	26754,	Seguence 26754, A	Sequence 727856,	Sequence 1, Appli
US-09-925-065A-821943	US-09-925-065A-561682	US-09-925-065A-561683	US-09-925-065A-111263	US-09-925-065A-899601	US-09-925-065A-899602	US-09-925-065A-233861	US-09-925-065A-233862	US-09-925-065A-3498	US-09-925-065A-652774	US-11-128-061-1855	US-11-128-061-5497	US-11-128-049-1855	US-11-128-049-5497	US-09-925-065A-875490	US-09-925-065A-34733	US-09-925-065A-713292	US-10-750-185-25879	US-10-750-623-25879	US-10-750-185-38674	US-10-750-623-38674	US-10-750-185-26754	US-10-750-623-26754	US-09-925-065A-727856	US-10-330-773-1
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63.4	63.4	63.4	63.4	62.8	62.8	62.8	62.8	62.8	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1
18.4	18.4	18.4	18.4	18.2	18.2	18.2	18.2	18.2	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18
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## ALIGNMENTS

US-10-514-878A-2

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Publication No. US20060035319A1

Publication No. US20060035319A1

GENERAL INFORMATION:

TITLE OF INVENTION: Disperainty the Particles

TITLE OF INVENTION: Preparing the Particles

SEQ ID NO 2

LENGTH: 1518

NUMBER OF SEQ ID NOS: 144; Score 24.2; DB 7; Length 1518;

Best Local Similarity 89.7%; Pred No. 0.72;

Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Mismatches
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Query Match 83.4%; Score 24.2; DB 7;
Best Local Similarity 89.7%; Pred. No. 0.72;
Matches 26; Conservative 0; Mismatches 3;
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Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             589 GATGGTGATATGGTTGATACTGGCTTTGG 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human papillomavirus US-10-514-878A-12
                                                                                                                                                                                                                                                                                                                83.4%;
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 89.7<sup>3</sup>
Matches 26, Conservative
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CITY: Washington
STATE: D.C.
  GENERAL INFORMATION:
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LENGTH: 1518
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TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
TITLE OF INVENTION: Preparing the Particles
FILE REFERENCE: 10/514,878
CURRENT APPLICATION NUMBER: US/10/514,878A
CURRENT FILING DATE: 2004-11-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Cape Town
TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
TITLE OF INVENTION: Preparing the Particles
FILE PERENCE: 10/514,878
CURRENT APPLICATION NUMBER: US/10/514,878A
CURRENT FILING DATE: 2004-11-16
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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                                                                                 Query Match 83.4%; Score 24.2; DB 7; Length 1518; Best Local Similarity 89.7%; Pred. No. 0.72; Matches 26; Conservative 0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10514878A Publication No. US20060035319A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10514878A Publication No. US20060035319A1 GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Human papillomavirus
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ORGANISM: Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human papillomavirus
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Matches 26; Conservative
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Matches 26, Conservative
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US-10-514-878A-10
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APPLICANT: University of Cape Town
TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and MeraITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles
TITLE OF INVENTION: Preparing the Particles
FILE REFERENCE: 10/514,878
CURRENT APPLICATION NUMBER: US/10/514,878A
CURRENT FILING DATE: 2004-11-16
SOFTHARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/10514878A
Publication No. US20060035319A1
GENERAL INFORMATION:
APPLICANT: University of Cape Town
TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Meighter Englishment of INVENTION: Preparing the Particles
FILE REPERENCE: 10/514,878
CURRENT APPLICATION NUMBER: US/10/514,878A
CURRENT FILING DATE: 2004-11-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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Publication No. US20050249745A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
HALLEK, Michael
TITLE OF INVENTION: PAPLILLOMA VIRUS CAPSOMERE VACCINE
TITLE OF INVENTION: PORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28

NUMBER OF SEQUENCES: 28

CORRESPEDINGE ADDRESS:
ADDRESSEE: FOLLEY & LARDNER
STREET: 3000 K Street, N.W.
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RESULT 10
US-11-098-686-6941/C
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LENGTH: 610
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PRILING DATE: 2000-12-4
PRIOR PRILING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-05-09
NUMBER OF SECIENT NUMBER: US 60/289,846
PRIOR PLING DATE: 2001-05-09
NUMBER OF SECIENT NUMBER: US 60/280,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 623;
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19.6; DE
Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 GATGCTGATATGCTTGATACTGGCTTTGG 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24.2;
Pred. No. 0.
                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SANdercock, COlin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEFANCE (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 809541, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/654,129
PILING DATE: 04-Sep-2003
                                         APPLICATION NUMBER: US/11/179,478
FILING DATE: 13-JULY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 84.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               1518 base pairs
                         LICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-925-065A-809541
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LENGTH: 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
.US-11-179-478-1
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Ubblication No. US2006024696A1

GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: NCLIEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING FILE REFERENCE: 09531-128001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Sequence 883719, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Indectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-130

PRIOR FILING DATE: 2001-01-130

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6941
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 87.5%;
Matches 21; Conservative
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US-09-925-065A-883719
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RESULT: 11

564 carccrcrcrcracararaccarr 589

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RESULT 14
US-11-098-686-9784
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JULIE OF INVENTION: US20040181048A1

SEQUENCE 575086, Application US/09925065A

PUBLICATION NO. US20040181048A1

GENERAL INFORMATION:
APPLICAMT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: NUALEOCIDE POLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US 60/255,065A

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-6

PRIOR FILING DATE: 2001-11-6

PRIOR FILING DATE: 2001-11-6

PRIOR FILING DATE: 2001-11-6

PRIOR FILING DATE: 2001-11-6

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR RELING DATE: 2001-01-6

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR APPLICATION NUMBER: US 60/289,846

NUMBER OF SEQ ID NOS: 95/086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.5%; Score 19; DB 6; Le
Best Local Similarity 75.9%; Pred. No. 1.1e+02;
Matches 22; Conservative 1; Mismatches 6;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 717454
LENGTH: 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-925-065A-717454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-925-065A-575086
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LENGTH: 617
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Sequence 9784, Application US/11098686

Publication No. US20060024696A1

GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TILLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFREENCE: 0933-1.28001

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: US 60/416,395

PRIOR APPLICATION NUMBER: US 60/416,395

PRIOR FILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 11433

SOFTWARE: FREEKEQ for Windows Version 4.0

SEQ ID NO 9784
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Sequence 762355, Application US/09925065A
Fublication No. Us20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-00-8
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-11-20
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2001-01-16
FRIOR APPLICATION NUMBER: US 60/250,766
FRIOR FILING DATE: 2001-01-16
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR APPLICATION NUMBER: US 60/260,766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 622;
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Pred. No. 1.1e+02
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Matches 22; Conservative
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Matches 22; Conservative
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US-09-925-065A-762355
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419 GCTGGTGATAGGGCAGATTCAGGAATT 445

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Sequence 18, Application US/10829826B
; Publication No. US20050266397A1
; GENERAL INFORMATION:
    APPLICANT: Boker, David J.
    APPLICANT: Blyn, Lawrence B.
    APPLICANT: APPLICANT: MASSITE, Christian
    TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF CORONAVIRUSES
    FILE REFERENCE: IBLS0075-100 (DIBLS-0058US)
    CURRENT APPLICATION NUMBER: US/10/829,826B
    CURRENT APPLICATION NUMBER: US/10/829,826B
    NUMBER OF SEQ ID NOS: 105
    SOFTWARE: FastSEQ for Windows Version 4.0
    SOFTWARE: PastSEQ for Windows Version 4.0
    SOFTWARE: PastSEQ for Windows Version 4.0
    SOFTWARE: Concavirus
    COGANTSM: Coronavirus
    COLETY MATCH
    SOFTWARE: PastSEQ for Windows Version 4.0
    SOFTWARE: PastSEQ f
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Post-processing:

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Run on:

The invention relates to a general primer or primer pair for amplifying and detecting or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPP) genotypes. The general primers are useful for amplifying cervical-neoplasia related HPV genotypes including

Claim 2; SEQ ID NO 8; 71pp; English.

AAV12162 AAV23923 AAV24099

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Result No.

AAX15111 AAX15112 AAZ40564

911 GCATCAGAGGTAACCATAGAACCACTAGG 883

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               papillomavirus sequence, encoding the Il capsid protein. The activity of nucleotide sequences of the invention may be described as virucidal and immunostimulantary. The isolated nucleotide sequence is useful in a method of producing a papillomavirus protein. The papillomavirus protein encoded by the nucleotide sequence is useful in the manifacture of a pharmaccutical composition for prophylactic treatment of cervical lesions and carcinomas caused by papillomavirus. Polynucleotides of the invention may be useful in vaccines or in gene therapy. The current sequence represents the HPV 16 Ll capsid protein gene SA-Ll-NLS (South African isolate)
oncogenic high-risk groups and low-risk groups. The general primers are useful for producing amplifying products to DNA of scores of diverse oncogenic HPV types and thus detecting the oncogenic HPV types in a sample but also to select cervical carcinoms and its pre-stage lesions at early stage by improving sensitivity according to HPV types. This sequence corresponds to PCR primer used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleotide sequence encoding papillomavirus protein, useful in the manufacture of a pharmaceutical composition for preventing cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a new isolated nucleotide sequence containing
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L1 capsid protein; HPV 16; virucide; immunostimulant; gene therapy; vaccine; cervical lesion; carcinoma; gene; ds.
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                                                                                                                                                                    ; Score 29; DB 12; Length 29; 
; Pred. No. 0.00036; 
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1452 BP; 458 A; 271 C; 281 G; 442 T; 0 U; 0 Other;
                                                                                                                                     Sequence 29 BP; 8 A; 7 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                                                                                                                                                                                                                                                                             GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPV 16 L1 capsid protein gene SA-L1-NLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williamson A;
                                                                                                                                                                                                                                                                                                                                                                        ACC47503/c
ID ACC47503 standard; DNA; 1452 BP.
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                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 29; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lesions and carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYCA-) UNIV CAPE TOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-290048/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ACC47503;
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Matches
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papillomavirus sequence, encoding the L1 capsid protein. The activity of nucleotide sequences of the invention may be described as virucidal and immunostimulantary. The isolated nucleotide sequence is useful in a method of producing a papillomavirus protein. The papillomavirus protein encoded by the nucleotide sequence is useful in the manufacture of a pharmaceutical composition for prophylactic treatment of cervical lesions and carcinomas caused by papillomavirus. Polynucleotides of the invention may be useful in vaccines or in gene therapy. The current sequence. represents the HPV 16 L1 capsid protein gene SAopt-L1-NLS (Optimised
                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleotide sequence encoding papillomavirus protein, useful in the manufacture of a pharmaceutical composition for preventing cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to a new isolated nucleotide sequence containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                   L1 capsid protein, HPV 16; virucide, immunostimulant, gene therapy; vaccine, cervical lesion, carcinoma, gene, ds.
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Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3,
                                                                                                                     HPV 16 L1 capsid protein gene SAopt-L1-NLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                                                                  Williamson A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCGTCAGAGGTTACCATAGAGCCACTAGG
                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 7; 36pp; English.
                               ACC47505 standard; DNA; 1452
                                                                                                                                                                                                                                                                                         30-AUG-2002; 2002WO-IB003531.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe sequence for HPV 16 L1.
                                                                                                                                                                                                                                                                                                                       31-AUG-2001; 2001ZA-00007228
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                                                                                       27-JUN-2003 (first entry)
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Best Local Similarity 89.7
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Varsani AD, Rybicki EP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lesions and carcinomas.
                                                                                                                                                                                                                                                                                                                                                     (UYCA-) UNIV CAPE TOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            South African isolate)
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                                                                                                                                                                                              Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-290048/28.
                                                                                                                                                                                                                            WO2003018623-A2
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12-OCT-1999
                                                                                                                                                                                                                                                            06-MAR-2003.
                                                            ACC47505;
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RESULT 3
ACC47505/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
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The patent discloses a chimeric protein comprising papillomavirus L1 or L2 protein and a biotin-binding polypeptide. Capsomere, papillomavirus or virus-like particle (VLP) comprising the chimeric protein is used for delivering a wide variety of biotinylated compounds e.g. proteins. Calls. The chimeric protein may also be used as a vaccine when the biotinylated substance is a viral antigon e.g. papillomavirus E2 or E7 proteins. It may be useful for treating tumours or other papillomavirus. Crelated lesions when the substance is a cytotoxin, chemocherapeutic agent, radioactive agent, or a gene encoding a cytokine or interleukin. The present sequence is a DNA encoding a chimeric protein 168 consisting of human papillomavirus 16 (HPV-16) mutant L1 protein fused to a biotinbinding peptide at the Cterminus. The L1 protein fused to a biotinbinding peptide at the Cterminus. The L1 protein fused from the wild-type sequence by deleting the amino acid Cys428. The modification of was done to prevent assembly of VLPs while allowing the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric biotin-binding human papillomavirus mutant L1 protein-169 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostátíc; antiviral; gene thěrapy; vaccíne; capsomere; VLP; virus-like particle; viral antigen; tumour; cytotoxin; cytokine; IL; interleukin; chemotherapeutic agent; radioactive agent; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric protein comprising a papillomavirus 11 or 12 protein and blocin-blanding polypetide, useful for delivering substances such proteins, nucleic acids and lipids into cells, particularly papillomavirus infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1500
/*tag= a
/product=:"Chimeric protein 169 containing human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ); DB 3; Length 1494; 0.18;
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                                                                                                                                                                                                                                                                                                           Velders MP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 15-18; 27pp; English.
                                                                                                                                                                                                                                                                                                        Nieland JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capsomeres at high efficiencies
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                                                                                           99WO-US027555
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Unidentified.
                                                                                                                                                                                99US-00413611
                                                                                                                                                                                                                                            (LOYO ) UNIV LOYOLA CHICAGO
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Atches 26; Conservative
                                                                                                                                                                                                                                                                                                        Mueller M, Kast WM,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-400041/34.
                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY71464
                                                                                           22-NOV-1999;
                                                                                                                                                       23-NOV-1998;
                                                                                                                                                                                   06-OCT-1999;
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AAD01238/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This nucleotide probe is specific for the HPV16 Human Papilloma Virus (HPV) gene. The degree of HPV infection can be assessed, by measuring the levels of expression of genes involved in the diseased state, and comparing the expression to each other or to reference genes. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric biotin-binding human papillomavirus mutant L1 protein-168 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapa
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papillomavirus 16 mutant Li protein fused to biotin-
binding peptide at the C-terminal"
1450. 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New method for assessing Human Papilloma Virus (HPV) infection by comparison of gene expression levels.
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/note= "Biotin-binding peptide DNA"
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Local Similarity 89.7%; Pred. No. 0.18
les 26; Conservative 0; Mismatches
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Unidentified.
assay; cancer; virus; HPV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                     Synthetic.
Human papillomavirus
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17-APR-1998;
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The sequences given in AAQ47166-67 encode the L1 capsid proteins from bovine and human papillomavirus respectively. These sequences may be inserted into a baculovirus transfer vector and operatively expressed by a promoter of the vector, and the capsid protein produced by transformed cells. The capsid protiens may be used in vaccines to induce high-titre neutralising antibody response in vertebrates. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L1; capsid protein; bovine; human; papillomavirus; baculovirus; transfer vector; promoter; capsid protein; transformation; vaccine; neutralising antibody; vertebrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                   Recombinant papilloma virus capsid proteins - for vaccines against papilloma virus and for diagnosis of virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24.2; DB 2;
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGTCAGAGGTTACCATAGAGCCACTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 35-37; 45pp; English.
                                                                                                                                                                                                                                                                        Kirnbauer R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ47166 standard; DNA; 1517 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-00941371.
                                                                                                                                      93US-00032869
                                                                                                                                                                                  92US-00941371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ## Match 83.4%; Local Similarity 89.7%; nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                        Lowy DR, Schiller JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine papillomavirus.
  Human papillomavirus.
                                                                                                                                                                                                                                                                                                                    WPI; 1993-249995/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          correct PF field.)
                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR38808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USN8032869-N.
                                            USN8032869-N
                                                                                                                                      16-MAR-1993;
                                                                                                                                                                                  03-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BPV1 L1 ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ47166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses a chimeric protein comprising papillomavirus il or il protein and a biotin-binding polypeptide. Capsomere, papillomavirus or virus-like particle (VLP) comprising the chimeric protein is used for delivering a wide variety of biotinylated compounds e.g. proteins a used for cells. The chimeric protein may also be used as a vaccine when the chimeric protein may also be used as a vaccine when the conjointylated substance is a viral antigen e.g. papillomavirus E2 or F2 proteins. It may be useful for treating tumours or other papillomavirus. C agent, radioactive agent, or a gene encoding a cytokine or interleukin. The present sequence is a DNA encoding a cytokine or interleukin. The present sequence is a DNA encoding a cytokine or interleukin. The present sequence is a DNA encoding a cytokine or interleukin. The present sequence is a DNA encoding a cytokine or interleukin. The present sequence is a DNA encoding a cytokine or interleukin. The present sequence is a DNA encoding a cytokine or interleukin. The present sequence by deleting the amino acid Cys428. The modification of was done to prevent assembly of VLPs while allowing the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric protein comprising a papillomavirus L1 or L2 protein and a biotin-binding polypeptide, useful for delivering substances such as proteins, nucleic acids and lipids into cells, particularly papillomavirus infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
papillomavirus 16 mutant L1 protein fused to biotin-
binding peptide at the C-terminal"
1450. .1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L1; capsid protein; bovine; human; papillomavirus; baculovirus; transfer vector; promoter; capsid protein; transformation; vaccine; neutralising antibody; vertebrate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.4%; Score 24.2; DB 3; Length 1500; ilarity 89.7%; Pred. No. 0.18; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1500 BP; 467 A; 291 C; 295 G; 447 T; 0 U; 0 Other;
                                                                                          /note= "Biotin-binding peptide DNA"
                                                                                                                                                                                                                                                                                                                                                                                     Velders MP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 20-23; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Mueller M, Kast WM, Nieland JD,
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ID AAQ47167 standard; DNA; 1517 BP.
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99US-00413611
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                                                                   *tag=
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY71465.
                                                                                                                                      WO200031128-A1
                                                                                                                                                                                                                            22-NOV-1999;
                                            misc_feature
                                                                                                                                                                                                                                                                      23-NOV-1998;
                                                                                                                                                                                                                                                                                             06-OCT-1999;
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21-JAN-1994
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RESULT 7

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Length 1517;

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Papillomavirus strain 16 (HPV16). This recombinant form of viral protein is capable of self-assembly into capsomer structures and viral capsids that comprise conformational antigenic epitopes can be used as a vaccine for the prevention or treatment of papillomavirus infections in vertebrates. The vaccine comprises a unit dose of a composition containing a self assembled HPV16 with at least 1 papillomavirus L1 conformational epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capsid protein; 11; HPV16; vaccine; prevention; treatment; self-assembly; viral protein; capsomer; capsid; antigenic epitope; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes the Li capsid protein from Human Papillomavirus strain 16 (HPV16). A recombinant form of this viral protein which is capable of self-assembly into capsomer structures and viral capsids that comprise conformational antigenic epitopes can be used as a vaccine for the prevention or treatment of papillomavirus infections in vertebrates. The vaccine comprises a unit dose of a composition containing a self assembled HPV16 with at least 1 papillomavirus Li conformational epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine against human papilloma virus - comprises HPV16 L1 polypeptide.
                                                                                                                                                                                                       Length 1517;
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                                                                                                                                                                      Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;
                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                   Score 24.2; DB 2;
Pred. No. 0.18;
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                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           BP
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                                                                                                                                                                                                                                                                                                                                                                                         AAV09855 standard; DNA; 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00475783
                                                                                                                                                                                                       83.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPV16 L1 capsid protein DNA.
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/product=
                                                                                                                                                                                                                                      26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus
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                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                        Matches
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AAV09855/
   *8888888888
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                                                                                                                                                               The sequences given in AAQ47166-67 encode the L1 capsid proteins from bovine and human papillomavirus respectively. These sequences may be inserted into a baculovirus transfer vector and operatively expressed by a promoter of the vector, and the capsid protein produced by transformed eells. The capsid protiens may be used in vaccines to induce high-ritre neutralising antibody response in vertebrates. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment; self-assembly;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine against human papilloma virus - comprises HPV16 Ll polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag="a
/product= "11"
/note= "partial recombinant capsid protein sequence"
                                                                                Recombinant papilloma virus capsid proteins - for vaccines against papilloma virus and for diagnosis of virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                       / Match 83.4%; Score 24.2; DB 2; Length 1517; Local Similarity 89.7%; Pred. No. 0.18; nes 26; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capsid protein; L1; HPV16; vaccine; prevention; treatme viral protein; capsomer; capsid; antigenic epitope; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPV16 recombinant L1 capsid protein DNA
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                                                                                                                                   Example 1; Page 32-34; 45pp; English
Kirnbauer R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lowy DR, · Schiller JT;
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93US-00032869
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Schiller JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-158363/14.
                                 WPI; 1993-249995/31.
                                                                                                                                                                                                                                                                                                                                      correct PF field.)
                                                  P-PSDB; AAR38807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW39904.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
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 Lowy DR,
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Matches
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Gaps

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3; Indels

29

Length 1517;

2;

83.4%; Score 24.2; DB 89.7%; Pred. No. 0.18; ive 0; Mismatches

26; Conservative

Matches

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ઠે 셤

Query Match Best Local Similarity

911 GCATCAGAGGTAACCATAGAACCACTAGG 883

ВР

AAV25817 standard; DNA; 1517

RESULT 12 AAV25817/ 10-JUL-1998 (first entry)

AAV25817;

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The present sequence represents the human papillomavirus proto-type HPV

16 L1 genome 5637-7155, from the present invention. The present invention

26 describes the immunisation of a host mammal against a papillomavirus

27 comprising administering to the host, according to an immunising

28 schedule, a self-assembled Human Papilloma Virus (HPV16) capsid (I)

29 containing at least 1 papillomavirus L1 conformational epitopes are produced by letting a

20 genetic construct comprising a papillomavirus L1 gene direct recombinant

21 cell by self-assembly of papillomavirus capsids containing a L1

22 polypeptide having an amino acid sequence encoded by the nucleic acid

23 polypeptide having an amino acid sequence encoded by the nucleic acid

24 polypeptide paving an amino acid sequence encoded by the nucleic acid

25 polyment of papillomavirus capsids containing a L1

26 polypeptide paving an amino acid sequence encoded by the nucleic acid

27 sequence given in the specification (see AAV25817). (I) are useful for

28 the diagnosis of and as vaccines for the prevention of papillomavirus

29 infections and their benign and malignant sequelae in vertebrates.

29 cused to produce remewable papillomavirus previence of any selected species

20 and type in cell culture. The self-assembled recombinant L1 capsid

20 protein has the efficacy of intext papillomavirus particles to induce

20 high levels of neutralising antiserum, in contrast to prior art L1

20 protein extracted from recombinant bacteria or denatured virions
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                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunisation of mammals and humans against papillomavirus infection comprises administering recombinant self-assembled capsid proteins
                        ö
                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus; HPV 16; L1 gene; immunisation; capsid;
                                                                                                                                                                                                                                                                                                                      Human papillomavirus proto-type HPV 16 L1 genome 5637-7155.
                                                                                                                                                                                                                                                                                                                                                                             conformational epitope; vaccine; sequelae; vertebrate; ss.
                        Indels
                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product= "HPV 16 L1 proto-type"
    Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "no stop codon given"
                      0; Mismatches
                                                                                   911 GCATCAGAGGTAAACCATAGAACCACTAGG 883
                                                             1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 17-20; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schiller JT, Kirnbauer R, Lowy DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. :1517
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing conformational epitopes.
                                                                                                                                                                                                   AAV25818 standard; DNA; 1517 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00475782.
89.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-00941371
93US-00032869
                                                                                                                                                                                                                                                                                 10-JUL-1998 (first entry)
                          26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-271010/24.
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW53487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5744142-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1998
                                                                                                                                                                                                                                          AAV25818;
                          Matches
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Human papillomavirus wild-type HPV 16 L1 conformational epitope gene.

Human papillomavirus, HPV 16; L1 gene; immunisation; capsid; conformational epitope; vaccine; sequelae; vertebrate; ss.

1. 1517 /\*teg= a /product= "HPV 16 L1 conformational epitope" /note= "no stop codon given"

Location/Qualifiers

Key

Human papillomavirus.

(USSH ) US DEPT HEALTH & HUMAN SERVICES. Schiller JT, Kirnbauer R, Lowy DR;

WPI; 1998-271010/24.

P-PSDB; AAW53486.

95US-00475782. 92US-00941371. 93US-00032869.

07-JUN-1995; 03-SEP-1992; 16-MAR-1993;

US5744142-A. 28-APR-1998.

```
The present sequence encodes the human papillomavirus HPV 16 Li
conformational epitope, from the present invention. The present invention
describes the immunisation of a host mammal against a papillomavirus
comprising administering to the host, according to an immunising
schedule, a self-assembled Human Papilloma Virus (HPV16) capsid (I)
containing at least 1 papillomavirus Li conformational epitope. The
papillomavirus Li conformational epitopes are produced by letting a
genetic construct comprising a papillomavirus Li gene direct recombinant
expression of the conformational epitope in a transformed eukaryotic host
expression of the conformational epitope in a transformed eukaryotic host
copypapitde having an amino acid sequence encoded by the nucleic acid
sequence given in the specification (present sequence). (I) are useful
for the diagnosis of and as vaccines for the prevention of papillomavirus
infections and their benign and malignant sequence of any selected species
used to produce renewable papillomavirus proteins are provided which can be
used to produce renewable papillomavirus reagents of any selected species
and type in cell culture. The self-assembled recombinant Li cappid
protein has the efficacy of intact papillomavirus particles to induce
thigh levels of neutralising antiserum, in contrast to prior art Li
protein extracted from recombinant bacteria or denatured virions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunisation of mammals and humans against papillomavirus infection comprises administering recombinant self-assembled capsid proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing conformational epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Col 21-24; 20pp; English.
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Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;

BP.

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Assay for papilloma virus - using antibody directed against recombinant
L1 polypeptide.
                                                                                                                                                                 Human; papillomavirus; bovine; L1 conformational protein; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                    Human papillomavirus prototype L1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 17-20; 34pp; English.
                                               AAV12162 standard; DNA; 1517
                                                                                                                                                                                    detection; diagnosis; ss.
                                                                                                                                                                                                               Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-109811/10.
P-PSDB; AAW44143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schiller JT,
                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1992;
16-MAR-1993;
                                                                                                      05-MAY-1998
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                                                                          AAV12162;
                                 AAV12162/c
                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An method has been developed for detecting papilloma virus in a specimen from a mammal. The method comprises contacting the sample with an antibody and detecting any antibody binding. The antibody is a polyclonal or monoclonal antibody produced by transforming a eukaryotic host cell with a genetic construct containing a papillomavirus L1 gene so that the cell expresses self-assembled papillomavirus-like particles containing at least 1 papillomavirus L1 conformational epitope. The present sequence encodes wild-type human papillomavirus L1 polypeptide. The method is for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assay for papilloma virus - using antibody directed against recombinant
L1 polypeptide.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                 Human; papillomavirus; bovine; L1 conformational protein; antibody; detection; diagnosis; 88.
                                                            ö
                               Length 1517;
Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the diagnosis of papillomavirus infections in mammals
                          Score 24.2; DB 2;
Pred. No. 0.18;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "no stop codon given"
                                                                                                           911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                                                                                          ATAGAGCCACTAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                       Human papillomavirus wild-type L1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Col 21-24; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowy
                                                                                                                                                                                 AAV12161/c
ID AAV12161 standard; DNA; 1517 BP.
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/*tag= a
/product= "L1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-00941371
93US-00032869
                            83.4%;
Local Similarity 89.7%;
hes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schiller JT, Kirnbauer R,
                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-109811/10.
P-PSDB; AAW44142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1992;
16-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5709996-A
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                                                                                                                                                                                                                             AAV12161;
                              Query Match
                                                            Matches
                                                                                                                                                                  RESULT 13
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Lowy DR;

Kirnbauer R,

/note= "no stop codon given"

95US-00472673 92US-00941371 93US-00032869

"11"

product=

Location/Qualifiers 1. .1517 /\*tag= a

```
An method has been developed for detecting papilloma virus in a specimen from a mammal. The method comprises contacting the sample with an antibody and detecting any antibody binding. The antibody is a polyclonal or monoclonal antibody produced by transforming a eukaryotic host cell with a genetic construct containing a papillomavirus Li gene so that the cell expresses self-assembled papillomavirus-like particles containing at least I papillomavirus Li conformational epitope. The present sequence encodes protocype human papillomavirus Li polypeptide. The method is for the diagnosis of papillomavirus infections in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                         83.4%; Score 24.2; DB 2; Length 1517;
89.7%; Pred. No. 0.18;
ive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV23923 standard; DNA; 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2003
10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV23923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
AAV23923/c
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Gaps

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3; Indels

DB 2; Length 1517;

Score 24.2; DB Pred. No. 0.18; 0; Mismatches

Query Match 83.4%; Best Local Similarity 89.7%; Matches 26; Conservative

911 GCATCAGAGGTAACCATAGAACCACTAGG 883

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1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29

```
This sequence encodes the human papillomavirus 16 (HPV16) L1 gene protein. The protein can be used in the method of the invention for detecting antibodies to a papilloma virus in a sample from a mammal. The method comprises: (a) providing self-assembled papillomavirus-like particles comprises at least one L1 conformational applilomavirus. The particles comprise at least one L1 conformational applitomavirus L1 gene to direct recombinant expression in a transformed eukaryotic host cell; (b) contacting the sample with the self-assembled papillomavirus-like particles; and (c) detecting any antibody binding to the self-assembled papillomavirus-like particles and c) detecting any entibod and the self-assembled for detecting antibodates to HPV16 as an indication of infection. (Updated on 17-OCT-2003 to standardise OS field)
                                              Human papillomavirus 16; HPV17; L1 gene; infection; antibody detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assay for antibodies to papilloma virus - using self-assembled papillomavirus-like particles comprising L1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 83.4%; Score 24.2; DB 2; Length 1517; Best Local Similarity 89.7%; Pred. No. 0.18; Matches 26; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;
                                                                                                                                 Location/Qualifiers
1. .1515
/*tag= a
/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 17-20; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                Kirnbauer R, Lowy DR, Schiller JT;
                                                                                                Human papillomavirus type 16.
                                                                                                                                                                                                                                                                                           95US-00472672.
                                                                                                                                                                                                                                                                                                                            92US-00941371
93US-00032869
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-321522/28.
P-PSDB; AAW54034.
              HPV16 L1 gene #1
                                                                                                                                                                                                                                                                                           1995;
                                                                                                                                                                                                                                                                                                                            03-SEP-1992;
16-MAR-1993;
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Gaps ö

Search completed: March 5, 2006, 22:12:08 Job time : 381.5 secs

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

**Database**:

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CZ3155950 CC Ba007
CZ315590 CC Ba007
CZ3156416 CC Ba025
CZ783180 CC Ba025
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CZ783180 CC Ba024
CG768184 TCB48.4 BA031646 Mus muscul
BR751 RPC111-30F1
BR208090 Danio rer
CC90324 t006115ba
BQ158020 NF015802P
BW938474 BW938474
BX208056 EST753340
CX505056 DAII XZG39
CZ507804 GRW2-1041
CZ505564 GRW2-1041
                                                                                                                                                                                                                                                                                                                                                                                                        DN408692 589 bp mRNA linear EST 07-MAR-2005
LIB4007-010-06-K1-B3 LIB4007 Canis familiaris cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Flssipedia, Canidae,
                                                                                                                                                                                                                                                                                                  CA495435 AGENCOURT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="LIB4007"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; k9
mesenteric lymphnode"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 8; Length 589;
Pred. No. 2.6e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymphnode"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staten, N.R.
Direct Submission (Staten, N.R.)
Unpublished (2005)
Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:9615"
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BG745404
BH457107
BH457107
BH321749
CZ735950
CZ73584166
CZ784184
CZ864166
CZ788184
CZ864166
CG78184380
CG78184180
CG78184180
CG78184434
BR71318620
BW9318474
BX213662
CK29626
                                                                                                                                                                                                                                                                                                                                                                                                                                   ZLN9364981, mRNA sequence
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                                                                                                                     4 0 1 0 6 0 7 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%;
82.1%;
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639
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752
795
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744
744
771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                 Canis.
Query Match
Best Local S:
Matches 23,
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AUTHORS
TITLE
JOURNAL
COMMENT
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DN408692
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BX227374 Danio rer
BX216514 Danio rer
AJ760626 AJ760826
AJ763893 AJ763893
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                                                                                         5, 2006, 21:59:29; Search time 3168 Seconds (without alignments) 428.291 Million cell updates/sec
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               5.1.7
Biocceleration Ltd.
                                                                                                                                                                                                                                             41078325 seqs, 23393541228 residues
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                                                                                                                                                                           1 gegtcagaggttaccatagagccactagg 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
              GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                    summaries
                                                                 nucleic search, using sw model
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DE105340
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CKZ60235
CKZ60232
CK260232
CR099508
CL110457
BZ161634
AQ993275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM529734
BM530649
CA875703
AJ730032
AZ501268
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Query
Match Length DB
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gb_est2:.*
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gb_gss1:.*
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Score

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Gerbera hybrid cv. 'Terra Regina'
Gerbera hybrid cv. 'Terra Regina'
Bukaryota, 'Vizidiplantae', Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicotyledons,
asterids; campanulids; Asterales; Asteraceae; Mutisioideae;
Mutisleae; Gerbera.

1 (bases 1 to 191)
Laitinen,R.A., Immanen,J., Auvinen,P., Rudd,S., Alatalo,E.R.,
Paulin,L., Ainasoja,M., Kotilainen,M., Koskela,S., Teeri,T.H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerbera hybrid cv. 'Terra Regina'
Gerbera hybrid cv. 'Terra Regina'
Gerbera hybrid cv. 'Terra Regina'
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
seterids; campanulids; Asterales; Asteraceae; Mutisioideae;
Mutisiaeae; Gerbera.
1 (bases 1 to 280)
Laitinen,R.A. Immanen,J., Auvinen,P., Rudd,S., Alatalo,E.R.,
Paulin,L., Ainasoja,M., Kotilainen,M., Koskela,S., Teeri,T.H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute of Biotechnology
Viikinkaari 9, P.O. Box 56, 00014 University of Helsinki, FINLAND.
Location/Qualifiers
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Genome Res. 15 (4), 475-486 (2005)
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'Terra Regina' cDNA clone
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/clone="G0000550010812F1"
/clone=type="leaf, transgenic line 35S-gaga2"
/clone_lib="G00005"

    191
/organism="Gerbera hybrid cv. 'Terra Regina'"

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    Indels
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Pred. No. 2.6e+02;
0; Mismatches 2;
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  Mismatches
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                                                                                                                                                                                                   AJ760626
AJ760626 G00005 Gerbera hybrid cv.
G0000500010E12F1, mRNA sequence.
                                                                                        568 gcgrcagracriaccacreagccacae 595
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/cultivar="Terra Regina"
                                              1 GCGTCAGAGGTTACCATAGAGCCACTAG 28
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Best Local Similarity 91.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Alatalo ER
    23; Conservative
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Direct Submission
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Numquery@sanger.ac.uk Unbublished
This sequence was generated from the T7 end of BAC 247D6. 247D6 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
Location/Qualifiers
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidenes; Cyprinidae; Danio.

1 (Dases 1 to 798)

Humphray,S.J., Huckle,E. and Durham,J.L.

Direct Submission

Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
BX227374 798 bp DNA linear GSS 29-JAN-2003 Danio rerio genomic clone DKEY-277E24, genomic survey sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
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BX216514
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Pred. No. 2.8e+02;
0; Mismatches 5; Indels
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKBY-277E24"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
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/note="vector pindigoBAC-536"
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/organism="Danio rerio"
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/db_xref="taxon:7955"
/clone="DKEY-247D6"
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Danio rerio
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82.1%;
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Best Local Similarity 82.13
Matches 23; Conservative
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BX216514
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Gaps

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
bcoRis Site_2: BcoRis Female C57BL/61 mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
BH10B electrocompetent cells (RRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU243490 Addaka eye CDNA library (SNKOl) Oryzias latipes CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: sanaka@bio.nagoya-u.ac.jp
This clone was isolated from Medaka eye cDNA library (SNK01) 5'end.
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/clone_lib="Medaka eye cDNA library (SNKO1)"
/note="Wild samples from Okayama Pref.(Southern part
Japan)"
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Sanaka, E., Hori, H., Naruse, K., Mitani, H. and Tanaka, M. Medaka EST analysis
Unpublished (2001)
Contact: Emi Sanaka
Department of Biological Sciences
Graduate School of Science, Nagoya University
Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.6%; Score 19.6; DB 1; Length 537;
84.6%; Pred. No. 4e+02;
tive 0; Mismatches 4; Indels (
                                                                                                                                                                                                          Length 486;
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Pred. No. 3.9e+02;
                                                                                                                                                                                                        ch 67.6%; Score 19.6; D
1 Similarity 84.6%; Pred. No. 3.9e
22; Conservative 0; Mismatches
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Oryzias latipes
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/strain="wild type"
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/tissue_type="eye"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGY33.03h, mRNA sequence.
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Fax: 81-52-789-2974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ221755 486 bp DNA linear GSS 14-JUN-2000 RPCI-23-50C11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-50C11, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 486)
Abao.S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M.,
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-50C11.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhaodtigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu, Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 50 row: C column: 11
                                                             Contact: Alatalo ER
Institute of Biotechnology
Viikinkaari 9, P.O. Box 56, 00014 University of Helsinki, FINLAND.
Location/Qualifiers
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinne; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                             1. .280
/organism="Gerbera hybrid cv. 'Terra Regina'"
                                                                                                                                                                                                                                                                                                                                                                                                                Length 280;
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
differentiation in Gerbera hybrida (Asteraceae)
Genome Res. 15 (4), 475-486 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                         ch 68.3%; Score 19.8; DB 1; 1 Similarity 91.3%; Pred, No. 2.8e+02; 21; Conservative 0; Mismatches 2;
                                                                                                                                                                                                     /mol_type="mRNA"
/cullivar="fers Regina"
/db_xref="taxon:226891"
/clone="G0000700010E06F1"
/tissue_type="early petal"
/dev_stage="1.4"
/clone_lib="G00007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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/strain="C57BL/6J"
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clone="RPCI-23-50C11"
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AZ221755.1 GI:8529804
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Best Local Similarity
Matches 21; Conserva
                                               15781570
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AZ221755
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Best Local Similarity 84.0.
Best Local 22, Conservative
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CV504457/c
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                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Raxi 301 838 0200
Raxi 301 838 0208
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 149 row: O column: 3
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Oryzias latipes DNA, forward end of BAC clone: Md0145B09, genomic
BEL05340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                     1 (bases 1 to 552)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M.,
Jong,P. and Fraser,C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Unpublished (1999)
Other GSSs: RPCI-23-14903.TV
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Oryzias latipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-14903"
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                                              Mus musculus (house mouse)
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  AZ256958.1 GI:9461222
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ilarity 84.6%;
Conservative 0
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                                                                    Mus musculus
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Best Local Similarity
Matches 22; Conserv
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REFERENCE

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/cissue_type="Floral buds"
//issue_type="Floral buds"
//lab_host="XL10-Gold"
//lab_host="Mixed Floral"
//lab_host="Wixed Floral"
//note="Vector: pluescript II SK(+) XR; Site 1: EcoRI;
//note="Vector: pupplier: Developmental series" Plants from pathogen-free Solanum tuberosoum var. Shepody, clone 176, nuclear stock were grown in a screenhouse under natural conditions. Developing floral buds were harvested at various sizes up to opening and pooled. RNA was isolated and used for library construction. A normalized library was constructed following a modified protocol of Bonaldo et al. (1996. Genome Research 6: 791-806)."
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Shimizu, N., Asakawa, S., Shimizu, A. and Sasaki, T.

The BAC end sequence of Oryaias latipes
Published Only in Database (2005)
2 (bases 1 to 601)
Shimizu, N., Asakawa, S., Sasaki, T. and Shimizu, A.
Direct Submission
Submitted (30-JUN-2005) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo, 160-8582, Japan (B-mall:nshimizu@dmb.med.keio.ac.jp,
Tel:81-3351-2370, Fax.81-3-3351-2370)
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1 (bases 1 to 613)
Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De Koeyer,D., Audy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S. Generation of ESTs from a normalized developing floral bud library Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Medaka HdrR BAC library"
/note="This sequence is forward end of BAC clone
Md0145B09."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 601;
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ON, E3B 6Z9, CANADA
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Pred. No. 4.1e+02;
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84.6%; Pred. No. 4.1e-
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryzias latipes"
/mol_type="genomic DNA"
/db_xref="taxon:8090"
/clone="Md0145B09"
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921 College Hill Rd, Fredericton, O
Email: bflinn@bioatlantech.nb.ca
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/clone="71003"
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/cultivar="Shepody"
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CK260232 790 bp mRNA linear EST 03-AUG-2004 EST706310 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAB294 3' end, mRNA sequence.
                             669 crcacacerrecrrrrcaccacrac 694
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Best Local Similarity
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VERSION
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CK260232
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                                                                                                                                                                                                                                                                               Sukaryotta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Wildiplantae, Streptophyta, Embryophyta, Tracheophyta, Stermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, asterids, lamids, Solanales, Solanaceae, Solanum.

1 (bases 1 to 765)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue Onpublished (2003)

Other ESTs: EST706310 EST706311 EST706312

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
Location/Qualifiers
                                Gaps
                               ö
Length 613;
                             Indels
Score 19.6; DB 7;
Pred. No. 4.1e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Solanum tuberosum"
                                                                                       149 Grcadaggrigcriringagccacrag 124
                                                           3 GTCAGAGGTTACCATAGAGCCACTAG 28
                                                                                                                                                                                                                                                 Solanum tuberosum (potato)
                                                                                                                                                                                                                        CK260235.1 GI:39817213
Query Match
Best Local Similarity 84.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                    Solanum tuberosum
                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                  RESULT 11
CK260235
                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                REFERENCE
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/done libe="potento abiotic stress cDNA library"
/done libe="potento abiotic stress cDNA; Site_2: Not; suppleter: Solamum tuberosum var. Kennebec plants were grown from cuttings on a l6hr light/8 hr dark cycle at 5 c for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants; Set 1 involved asturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed alpants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and hear stressed roots were harvested at 6 hr, 12 hr, 1 d, at the were one tressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and hear stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and hear stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and hear stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d rom each tissue and stress was pooled to construct the cDNA library. RNA sample."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="abiotic stress treated leaf and root tissue"
                                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids; lamiids, Solanales, Solanaceae, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/.
                                                                                                                                                                                                                                                                 1 (bases 1 to 790)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Other_ESTs: EST706311 EST706312 EST706313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 67.6%; Score 19.6; DB 7; Similarity 84.6%; Pred. No. 4.3e+02; 22; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         669 GTCAGAGGTTGCTTTTGAGCCACTAG 694
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clone="POAB294"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                             Solanum tuberosum (potato)
CK260232.1 GI:39817210
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Gaps ;

Query Match 67.6%; Score 19.6; DB 7; Length 765; Best Local Similarity 84.6%; Pred. No. 4.2e+02; Matches 22; Conservative 0; Mismatches 4; Indels

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/clone lib="MHPP"
                                                                                  Best Local Similarity
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                                                              Query Match
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                   RESULT 15
CL110457
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3 Cciurognathi; Muroidea; Muridae; Murinae; Mus.

4 (bases 1 to 838)

Adams.D.J., Biggs, P.J., Cox.A.V., Davies, R.M., van der Weyden, L., Jonkersi, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.

Direct Submission

Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                DB114072 803 bp DNA linear GSS 02-AUG-2005 Oryzias latipes DNA, forward end of BAC clone: Md0158G03, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                  Shimizu,N., Asakawa,S., Shimizu,A. and Sasaki,T.

Published only in Database (2005)
2 (Dases 1 to 803)
Shimizu,N., Asakawa,S., Sasaki,T. and Shimizu,A.

Shimizu,N., Asakawa,S., Sasaki,T. and Shimizu,A.

Submitted (30-UNW-2005) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo, 160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 05-JUL-2004
                                                                                                                                                                                                                             Oryzias laripes
Oryzias laripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acauthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR099508 838 bp DNA linear GSS 05-JUL-200
Forward strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHPP279f02, genomic survey sequence.
CR099508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryzias latipes"
/mol_type="qenomic DNA"
/db_xref="taxon:8090"
/clone="Md0158G03"
/clone=lib="Medaka HdrR BAC library"
/note="This sequence is forward end of BAC clone Md0158G03."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.6%; Score 19.6; DB 11; Length 803; 84.6%; Pred. No. 4.3e+02;
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GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                              Oryzias latipes (Japanese medaka)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .838
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 GAGTCAGTGGTTTCCATAGAGACACT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP279f02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCGTCAGAGGTTACCATAGAGCCACT 26
                                                                                                                                                                  DE114072.1 GI:71633484
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Matches 22, Conservative
                                                                                                                         survey sequence.
DE114072
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                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
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AUTHORS
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CR099508
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KEYWORDS
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                                         RESULT 13
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                                                            DE114072
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                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Xenopus tropicalis

Xenopus tropicalis

Ambhibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

I (bases I to 990)

Xremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)

Contact: Richard K wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .990 //
Organism="Xenopus tropicalis"
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/doc_type="genomic DNA"
/clone="ISB1-53J18"
/clone="ISB1-53J18"
/clone="Jb="ISB1"
/note="WetCr: pBeloBAC11; ISB-1 Xenopus tropicalis BAC Library Segment 1"
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                                                                       Gape
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               Score 19.6; DB 11; Length 838; Pred. No. 4.3e+02;
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67.6%; Score 19.6; DB 10; Length 990;
Best Local Similarity 84.6%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Sequencing Center
Washington University School of Medicine
Email: submissionsewatson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTATAGGG
Class: BAC ends
High quality sequence start: 75
High quality sequence stop: 773.
67.6%; Scott No. 84.6%; Pred. No. 84.6%; O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: March 5, 2006, 23:58:01
                                                                                                                     4 TCAGAGGTTACCATAGAGCCACTAGG
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CL110457.1 GI:40604092
                                                                     22; Conservative
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Appli Appli Appli Appli Appli

Sequence Sequence

Sequence

Appl Appl Appl Appli Appli

Sequence

Sequence

Sequence Seguence Sequence Sequence Sequence

Sequence Sequence

Sequence

OM nucleic

Run on:

Sequence:

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Sequence 2, Application US/09210168
| Patent No. 6355424
| GENERAL INFORMATION: Attila T. |
| TITLE OF INVENTION: ASSESSMENT OF HUMAN PAPILLOMA VIRUS-RELATED DISEASE |
| TITLE OF INVENTION: ASSESSMENT OF HUMAN PAPILLOMA VIRUS-RELATED DISEASE |
| TITLE OF INVENTION: ASSESSMENT OF HUMAN PAPILLOMA VIRUS-RELATED DISEASE |
| FILE REFERENCE: 26294005402
| CURRENT PILING DATE: 1998-12-11 |
| PRIOR PAPLICATION NUMBER: U.S. 60/082,167 |
| PRIOR PAPLICATION NUMBER: U.S. 60/070,486 |
| PRIOR PAPLICATION NUMBER: U.S. 60/069,426 |
| PR
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APPLICANT: Mueller, Martin
APPLICANT: Kast, Wijbe
APPLICANT: Nieland, John
APPLICANT: Nieland, John
APPLICANT: Velders, Markwin
TITLE OF INVENTION: Chimeric Biotin-Binding Papillomavirus Protein
FILE REFERENCE: 202325
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Pred. No. 0.076;
0; Mismatches 3;
US-09-319-056B-12
US-08-578-634C-1
US-08-815-667-8
US-08-815-667-8
US-08-409-122-1
US-08-913-644-1
US-09-319-056B-13
US-09-319-056B-15
US-09-319-056B-16
US-09-319-056B-18
US-09-319-056B-18
US-09-319-056B-18
US-09-319-056B-18
US-09-628-099-28
US-09-628-099-28
US-09-628-099-28
US-10-056-360-38
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US-05-413-611A-5/c
; Sequence 5, Application US/09413611A
; Patent No. 6380364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human papillomavirus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
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     383
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                                                                                                                                                                           March 5, 2006, 19:08:04 ; Search time 80.5 Seconds (without alignments) 640.364 Million cell updates/sec
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                            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: /cgn2 6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2 6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2 6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2 6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2 6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2 6/ptodata/1/ina/H_COMB.seq:*
7: /cgn2 6/ptodata/1/ina/PP_COMB.seq:*
7: /cgn2 6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2 6/ptodata/1/ina/PP_COMB.seq:*
9: /cgn2 6/ptodata/1/ina/PP_COMB.seq:*
9: /cgn2 6/ptodata/1/ina/PP_COMB.seq:*
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US-09-319-056B-10
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Maximum DB
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CORRESPONDENCE ADDRESS:
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, LOCATION: 1...1
US-08-032-869A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
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                                                                                                                                                                                                            CTHER INFORMATION: Description of Artificial Sequence:biotin-binding
CTHER INFORMATION: papillomavirus protein 168
NAME/KEY: CDS
LOCATION: (1)..(1491)
US-09-413-611A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:biotin-binding OTHER INFORMATION: papillomavirus protein 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mueller, Martin
APPLICANT: Kast, Wijbe
APPLICANT: Kast, Wijbe
APPLICANT: Nieland, John
TITLEOF INVENTION: Chimeric Biotin-Binding Papillomavirus Protein
FILE REPERENCE: 20235
CURRENT APPLICATION NUMBER: US/09/413,611A
CURRENT FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 60/109,510
PRIOR PILING DATE: 1999-11-23
WUMBER OF SEC ID NOS: 8
SOFTWARE: PatentIN Ver. 2.0
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Pred. No. 0.076;
0; Mismatches 3; Indels 0
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89.7%; Pred. No. 0.076;
tive 0; Mismatches 3; Indels 0
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Patent No. 5437951
GENERAL INFORMATION:
APPLICANT: Lowy, Douglas R.
APPLICANT: Schiller, John T.
APPLICANT: Strinbauer, Reinhard
TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
CURRENT FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 60/109,510
PRIOR FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 5
LENGTH: 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09413611A
Patent No. 6380364
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Query Match 83.4%;
Best Local Similarity 89.7%;
Matches 26; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 89.77
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (1)..(1497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-032-869A-1/c
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LENGTH: 1500
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ADDRESSER KROBEE, MARTENS, OLSON & BEAR

STREET: 630 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach

GOUNTHS: CA

STREET: 630 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach

COMPANDED: APPRINGING

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Length 1517;
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APPLICANT: Schiller, John T.
APPLICANT: Kirnbauer, Reinhard
TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
TITLE OF INVENTION: PAPILLOWAVIRUS CAPSID PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, WARTENS, OLSON & BEAR
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/08/472,673
FILING DATE: 07-JUN-1995
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: US 08/032,869
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 07/941,371
FILING DATE: 03-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                           NIH032.001CP1
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                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ONGINNL SOURCE:
ORGANISM: Human papillomavirus
STRAIN: HPV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-08-472-673-2/c
; Sequence 2, Application US/08472673
; Patent No. 5709996
                           REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
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                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
                                                                                                                                                                LENGTH: 1517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                            TELEPAX: 619-235-0176
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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, LOCATION:
US-08-472-673-1
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89.7%; Pred. No. 0.076;
tive 0; Mismatches 3; Indels 0
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APPLICANT: Lowy, Douglas R.
APPLICANT: Schiller, John T.
APPLICANT: Schiller, John T.
APPLICANT: SCHILLER, Reinhard
TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
NUMBER OF SCHINCES: 6
CORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: KNOBBE, MARTENS, OLSON & BEAR
STREET: SCO NOWPORT Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,673
FILING DATE: 07-UNN-1995
CLASSIFICATION: 435
YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/032,869A
FILING DATE: 16-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,371
FILING DATE: 03-SEP-1992
ATTORNEY AGENT INFORMATION:

NAME: Kirpatrick Ph.D., Anita M.
REGISTRATION NUMBER: 3,617
REGISTRATION NUMBER: 140,617
REFERENCE/DOCKET NUMBER: 141,032.001CP1
TELEPHONE: 619-235-8550
TELEPHONE: 619-235-856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1517 base pairs
TYPE: nucleic acid
STRANDEDNESS: 6110316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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APPLICATION NUMBER: US 08/032,869
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: US 07/941,371
FILING DATE: 03-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kirkpatrick Ph.D., Anita M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08472673
Patent No. 5709996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.77
Matches 26; Conservative
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; LOCATION: 1...1
US-08-032-869A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NAMI-SENSE: NO
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US-08-472-673-1/c
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                                                                                                                                                                                                                                                  RESULT 9
US-08-475-782-2/c
; Sequence 2. Application US/08475782
; Patent No. 5744142
; Patent No. 5744142
; GENERAL INFORMATION:
; APPLICANT: Lowy, bouglas R.;
; APPLICANT: Schiller, John T.;
; APPLICANT: Kirnbauer, Reinhard
; TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
; TITLE OF INVENTION: PAPILLOWAVIRUS CAPSID PROTEINS;
NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSE: KNOBBE, MARTENS, OLSON & BEAR
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PacentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,782
FILING DATE: 07-JUN-195
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/032,869
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: US 08/032,869
FILING DATE: 03-SEP-1992
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 32,617
REFERENCE/DOCKET NUMBER: 32,617
REFERENCE/DOCKET NUMBER: NIH032.001CP1
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-235-8550
TELEFAX: 619-235-8550
TELEFAX: 619-235-8550
TELEFAX: 619-235-8550
TELEFAX: 619-235-8550
TELEFAX: FRARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                             0; Mismatches
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MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
                                                                                        Query Match
Best Local Similarity 89.7
Matches 26; Conservative
                                       LOCATION: 1..1517
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USA
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; LOCATION:
US-08-475-782-2
                                           ;
US-08-475-782-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                      83.4%; Score 24.2; DB 2; Length 1517; 89.7%; Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                              us-08-475-782-1/c

Sequence 1, Application US/08475782

Fatent No. 5744142

GENERAL INFORMATION:

APPLICANT: Lowy, Douglas R.

APPLICANT: Schiller, John T.

APPLICANT: Schiller, John T.

TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT

TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR

STREET: 620 Newport Center Drive, Sixteenth Floor

CITY: Newport Beach

COUNTRY: USA

ZIP. ACC
                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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STRANDEDNESS: single
TOPCLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                       Best Local Similarity 89.7 Matches 26; Conservative
                                                                                                                                                                                      1..1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
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ANTI-SENSE: N
                                                                                                                                                               NAME/KEY:
; LOCATION:
US-08-472-673-2
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Gaps

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TITLE OF INVENTION: SELP- ASSEMBLING RECOMBINANT
TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROOBBE, MARTENS, OLSON & BEAR
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
TREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lowy, Douglas R.
APPLICANT: Schiller, John T.
APPLICANT: Kirnbauer, Reinhard
TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT
TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLINICATION NUMBER: US/08/472,678
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24.2; DB 2;
Pred. No. 0.076;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/032,869A
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: US 07/941,371
FILING DATE: 03-8EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kirkpetrick Ph.D., Anita M.
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: NIH032.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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                                                                                                                                                                                                              ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-484-503-1/c
; Sequence 1, Application US/08484503
; Patent No. 5985610
Kirnbauer, Reinhard
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1517 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative (
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STRANDEDNESS:
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; LOCATION:
US-08-472-678-2
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                                                                                                                                                                   STATE: C. COUNTRY:
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                                                       APPLICANT: Lowy, Douglas R.
APPLICANT: Schiller, John T.
APPLICANT: Kirnbauer, Weinhard TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT TITLE OF INVENTION: PAPILLOMAVIRUS CAPSID PROTEINS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBRF ...
                                                                                                                                                                                                                                          AUDRESSEE: KNOBBE, MARTENS, OLSON & BEAR STREET: 620 Newport Center Drive, Sixteenth Floor STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kirkpatrick Ph.D., Anita M.
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: NIH032.001CP1
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/032,869A
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: US 07/941,371
FILING DATE: 03-SEP-1992
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRAIN: HPV16
                                                  Sequence 1, Application US/08472678
Patent No. 5871998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08472678
Patent No. 5871998
GENERAL INFORMATION
APPLICANT: Lowy, Douglas R.
APPLICANT: Schiller, John T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1517 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619-235-0176
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.4
Best Local Similarity 89.7
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 1..1517
US-08-472-678-1
                                                                                                                                                                                                                                                                                                                                        CA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-472-678-2/c
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Length 1517;

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83.4%; Score 24.2; DB 2; Length 1517;
89.7%; Pred. No. 0.076;
tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-944-368A-1/C
; Sequence 1, Application US/08944368A
; Sequence 1, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
; TITLE OF INVENTION: Pormulations and Methods of Use
; TITLE OF INVENTION: Pormulations and Methods of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Borun

>>2 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago Sypyre: Illinois COUNTRY: United States of America COUNTRY: Illinois ZIP: 60606-6402 COMPUTER READABLE FORM: MEDLUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/944,368A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 233 South Wacker Drive, 6300 Sears Tower CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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APPLICATION NUMBER: 08/032,869
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ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27013
                                                                               ALICKNEH, MAME: KIKEPATICK Ph.D., Anite REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET VUMBER: NIHO: TELECOMUNICATION INFORMATION: TELEPHONE: 619-235-0176
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1517 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECONMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1518 base pairs
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Best Local Similarity 89.79
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
LOCATION:
US-08-484-503-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Separate | Separation | Separ
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                       APPLICATION NUMBER: 05/06/101/2018
CLASSIFTCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE:
ATTORNEY/AGRIT INFORMATION:
NAME: Kirkpatrick Ph.D., Anita M.
REGISTRATION NUMBER: 32,617
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: NIH032.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEPHONE: 619-235-8550
TELEPHONE: 619-235-8056
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 13:17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: NICHEL TYPE: NOA (Genomic)
HYPOTHETICAL: NO
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APPLICATION NUMBER: US/08/484,503
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human papillomavirus
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: 1..1
US-08-484-503-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN: HPV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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ANTI-SENSE: N
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                                                                                                                                                                  Query Match 83.4%; Score 24.2; DB 3; Length 1518; Best Local Similarity 89.7%; Pred. No. 0.076; Matches 26; Conservative 0; Mismatches 3; Indels 0
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US-09-820-764-1/c
| Sequence 1, Application US/09820764
| Patent No. 6352696
| GENERAL INFORMATION:
| APPLICANT: BURGER, Alexander
| HALLEK, Michael
| TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCES:
ADDRESSE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2000-5109
COMPUTER: TOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: DAN PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 30-Mar-2001
CLASSIFICATION CURRENT APPLICATION CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APP
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REGISTRATION NUMBER: 31,298
REFERENCE DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPHONE: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COCATION: 1..1515
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-820-764-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 1518 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
    CDS
1..1518
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; NAME/KEY:
; LOCATION:
US-08-944-368A-1
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Search completed: March 5, 2006, 19:13:35 Job time: 80.5 sec8

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us-10-720-424b-8.rnpbm

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5, 2006, 22:00:24; Search time 361 Seconds (without alignments) 664.299 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19587084
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                   1 gegtcagaggttaccatagagccactagg 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Applications_NA_Main:*
                                                                                                                                                                                                                                                                                     9793542 segs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 - nucleic search, using sw model
                                                                                                                                                                                                                                   IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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29
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Match Length
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                                                                                                  March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score .
                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                     Scoring table:
                                                                 OM nucleic
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                                                                                                                                                                                                    Sequence:
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                                                                                                  Run on:
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Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence .09-162-904A-1

Sequence 1, Sequence 3,

Sequence Sequence

12-526A-1

Sequence Sequence Sequence Sequence

68-046-1

Sequence Sequence Sequence

equence equenc	ddv 'oc* annan	DETECTING DIVERSE GENOTYPES	Length 29; Indels 0; Gaps 0;	. *
9 US-10-918-337-11 9 US-10-918-337-11 9 US-10-367-057-115 9 US-10-494-800-2 1 US-10-494-800-2 1 US-10-43-911-1 9 US-10-978-239-14 8 US-10-978-248-9 5 US-10-925-055A-151425 9 US-10-367-057-127 9 US-10-367-057-127 1 US-10-056-359-28 1 US-10-056-359-28 5 US-10-056-360-30 5 US-10-056-360-30 9 U	•	ND PROCESS FOR 1872 BY PCR 424B 775370	O%: Score 29; DB 8; Le O%: Pred. No. 0.00072; O; Mismatches O; ATAGAGCCACTAGG 29 	//10487719 435Al dd rrd nna-Lise
C 24 24.2 83.4 1518 C 25 24.2 83.4 1518 C 26 24.2 83.4 1596 C 27 24.2 83.4 1596 C 29 22.6 77.9 1421 C 31 20.6 77.9 1420 C 33 20.8 77.7 24 C 33 20.6 77.9 1420 C 33 20.6 77.9 1420 C 33 19.6 67.6 398 C 37 19.6 67.6 398 C 37 19.6 67.6 398 C 40 19.4 66.9 1404 C 41 19.4 66.9 1808	18.6 64.1	RESULT 1 US-10-720-424B-8 Sequence 8, Application US/10720424B PUD1ication No. US20040248085A1 GENERAL INFORMATION: APPLICANT: Lee, Sang-wha APPLICANT: Lee, Sang-wha APPLICANT: Kim, Yeon-Soo APPLICANT: Kim, Yeon-Soo APPLICANT: Kim, Yeon-Soo APPLICANT: Kim, Senug-Vol APPLICANT: Him, Yeon-Soo TITLE OF INVENTION: HUWAN PAPILLOMAVIRUS BY PCR FILE REFERENCE: NEITO018 CURRENT APPLICATION NUMBER: US/10/720,424B CURRENT FILING DATE: 2003-11-24 PRIOR APPLICATION NUMBER: KR10-2002-0075370 PRIOR APPLICATION NUMBER: KR10-2003-0053147 PRIOR APPLICATION NUMBER: KR10-2003-0053147 PRIOR APPLICATION NUMBER: RAIO-2003-0053147 SOFTWARE: PatentIn version 3.2 SEQ ID NO 8 IENGTH: 29 IENGTH: 29 IENGTH: 40	Query Match Best Local Similarity 100 Matches 29; Conservative Oy 1 GCGTCAGAGGTDACC/ Db 1 GCGTCAGAGGTTACC/	RESULT 2 US-10-487-719-2/c Sequence 2, Application US/1048771; Publication No. US20050090435A1; GENERAL INFORMATION: APPLICANT: Varsani, Arvind; APPLICANT: Tybicki, Edward; APPLICANT: Williamson, Anna-Lise

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ASSESSMENTS OF HUMAN PAPILLOMA VIRUS-RELATED DISEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: KNOBBE, MARTENS, OLSON & BEAR
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY. Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT PAPILLOMAVIRUS CAPSID PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; DB 3;
0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: NIH032.001CP1
                       TITLE OF INVENTION: ASSESSMENTS OF HUMAN PAP.
FILE REFERENCE: 2629-40501054
CURRENT APPLICATION NUMBER: US/09/970,477
CURRENT FILING DATE: 2001-10-04
PRIOR PLICATION NUMBER: U.S. 09/210,168
PRIOR APPLICATION NUMBER: U.S. 60/082,167
PRIOR APPLICATION NUMBER: U.S. 60/082,167
PRIOR PILING DATE: 1998-04-17
PRIOR PILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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REPLICATION NUMBER: US/09/832,065
FILING DATE: 09-Apr-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/316,487

PILING DATE: «Unknown-
ATTORNEY/AGENT INFORMATION:

NAME: Kirkpatrick Ph.D., Anita M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24.2;
Pred. No. 0.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Schiller, John T.
Kirnbauer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
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Publication No. US20030050439A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619-235-0176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: L1-HPV16
US-09-970-477-2
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Publication No. US20050090435A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tybicki, Edward
APPLICANT: Tybicki, Edward
APPLICANT: Tybicki, Edward
APPLICANT: Tybicki, Edward
APPLICANT: Williamson, Anna-Lise
TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and
TITLE OF INVENTION: Pharmaceutical Compositions and TITLE OF INVENTION: Pharmaceutical Compositions for Prophylactic Treatment of
TITLE OF INVENTION: Leaions and Carcinomas
TITLE FERRENCE: 022455-116
CURRENT FILING DATE: 2004-02-27
PRIOR PILING DATE: 2002-08-30
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and TITLE OF INVENTION: Isolating Said Pharmaceutical Compositions, and Use of Said TITLE OF INVENTION: Pharmaceutical Compositions for Prophylactic Treatment of TITLE OF INVENTION: Desions and Carcinomas for Prophylactic Treatment of FILE REFERENCE: 025455-116
CURRENT PAPLICATION NUMBER: US/10/487,719
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: PCT/1802/03531
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 1452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.4%; Score 24.2; DB 9; Length 1452; 89.7%; Pred. No. 0.25; ive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: fragment of L1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: fragment of L1 gene US-10-487-719-2
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.73
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 89.7
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-10-487-719-4/C
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US-09-970-477-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-487-719-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Sequence 2, Application US/09970477 Patent No. US20020127545Al GENERAL INFORMATION:

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Gaps

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CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/371,846
FILING DATE: 21-Feb-2003
CLASSIFICATION: CLASSIFICATION
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10371846
Publication No. US20030219873A1
GENERAL INFORMATION:
APPLICANT: Lowy, Douglas R.
Schiller, John T.
Kirnbauer, Reinhard
TITLE OF INVENTION:
PAPILLOMAVIRUS CAPSID PROTEINS
                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.4%; Score 24.2; DB 6; Best Local Similarity 89.7%; Pred. No. 0.25; Matches 26; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: NIH032.001CP1
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APPLICATION NUMBER: US/08/032,869
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: US 07/941,371
FILING DATE: 03-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kirkpatrick Ph.D., Anita M.
REGISTRATION NUMBER: 32,617
                                                                                                  0; Mismatches
                                                                                                                                                                                        911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                                                    Score 24.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..1517
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-235-0176 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Newport Beach
                                                 Query Match 83.4
Best Local Similarity 89.7
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN: HPV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
     US-09-832-065-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-371-846-1
                                                                                                                                                                                                                                                                                                                                                Query Match 83.4%; Score 24.2; DB 3; Length 1517; Best Local Similarity 89.7%; Pred. No. 0.25; Matches 26; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delication No. Colors

GENERAL INFORMATION:
APPLICANT: Lowy, Douglas R.
Schiller, John T.
Kirnbauer, Reinhard
TITLE OF INVENTION: SELF-ASSEMBLING RECOMBINANT
PAPILLOMAVIRUS CAPSID PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/832,065
FILING DATE: 09-Apr-2001
CLASSIFICATION NUMBER: US/09/832,065
FILING DATE: 09-Apr-2001
CLASSIFICATION NUMBER: 09/316,487
PILING DATE: -UNKNOWN-
ATTORNEY/AGENT INFORMATION:
NAME: Kirkpatrick Ph.D., Anita M.
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: NIH032.001CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                                                                                                                                            ORGANISM: Human papillomavirus
STRAIN: HPV16
                                                                                                                                                                                                                                                  LOCATION: 1..1517
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..1517
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09832065
Publication No. US20030050439A1
                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                        HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-832-065-2/c
                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                 US-09-832-065-1
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HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09162904A Patent No. US20020168372A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1518 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Durst, Matthias
APPLICANT: Gissmann, Lutz
                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-09-162-904A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/371,846
FILING DATE: 21-Feb-2003
FILING DATE: 21-Feb-2003
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: KNOBBES, MARTENS, OLSON & BEAR
STREET: 620 Nowport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                APPLICANT: Lowy, Douglas R.
Schiller, John T.
Kirnbauer, Reinhard
TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
PAPILLOMAVIRUS CAPSID PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: NIH032.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-6850
TELEFRX: 619-235-0176
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/032,869
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: US 07/941,371
FILING DATE: 03-SEP-1992
911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             911 GCATCAGAGGTAACCATAGAACCACTAGG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kirkpatrick Ph.D., Anita M.
REGISTRATION NUMBER: 32,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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                                                                                                                                    Sequence 2, Application US/10371846
Publication No. US20030219873A1
GENERAL INFORMATION:
APPLICANT: Lowy, Douglas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09820765
Publication No. US20020039584A1
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APPLICANT: BURGER, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                   US-10-371-846-2/c
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APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
TITLE OF INVENTION: 0848-068-999
CURRENT ELLING DATE: 1998-09-29
CURRENT FILING DATE: 1998-09-29
PRIOR PILING DATE: 1997-06-27
PRIOR FILING DATE: 1996-05-01
PRIOR PLING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/641,570
PRIOR PLING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/641,570
PRIOR PLING DATE: 1996-05-01
PRIOR PLING DATE: 1996-05-01
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                                                                                                 COMPUTE: MESLILISCOLI
COUNTRY: U.S.A.

ZUP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRIT APPLICATION DATE: 30-Max-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: «Unknown»
PRIOR APPLICATION UNMBER: US 09/026, 896
FILING DATE: 20-PEB-1998
ATTORNEY AGENT INPORMATION:
NAME: SanderCOCK, Colin G.
REFERENCE/DOCKET NUMBER: 31.298
REFERENCE/DOCKET NUMBER: 37067/102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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83.4%; Score 24.2; DB 3;
Best Local Similarity 89.7%; Pred. No. 0.25;
Matches 26; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 1..1515
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-820-765-1
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY & LARDNER
STREET: 3000 K Street, N.W
CITY: Washington
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COMPUTER: INP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: 07-No. US20030021806A1-2001
CLASSIFICATION: <UNKnown>
                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCII FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 83.4%; Score 24.2; DB 3; Best Local Similarity 89.7%; Pred. No. 0.25; Matches 26; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                 NAME: Sandercock, Colin G.
REGIGSTRATION NUMBER: 31.298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..1515
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3000 K.Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                        (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09986118A Publication No. US20010021806A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                    FILING DATE: 1998-02-20 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1518 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BURGER, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 672-5
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-986-118A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-017-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                               PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of L1 gen
1 OTHER INFORMATION: HPV16 DNA clone P114/16/2
US-09-162-9044-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Mucleotide sequence of L1 ger
; OTHER INFORMATION: HPV16 DNA clone P114/16/11
US-09-162-904A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INC. 03.02202203.741.

GENERAL INC. 03.02202203.741.

APPLICANT: Durst, Matthias

APPLICANT: Durst, Matthias

APPLICANT: GISSGMAIN. Lutz

TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOWAVIRUS L1 PROTEIN CAPABLE

TITLE OF INVENTION: OF FFFICIENTLY FORMING VIRUS-LIKE PARTICLES

FILE REFERENCE: 8484-068-999

CURRENT APPLICATION NUMBER: US/09/162,904A

CURRENT FILING DATE: 1998-09-29

FRIOR FILING DATE: 1997-06-27

PRIOR FILING DATE: 1997-06-27

PRIOR FILING DATE: 1996-05-01

PRIOR FILING DATE: 1996-05-01

PRIOR FILING DATE: 1993-07-16

NUMBER OF SEQ ID NOS: 6

SOCTWARE: Patentin version 3.1

SEQ ID NO 2: LENGTH: 1518
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                                                                                                                                                                            Score 24.2; DB 3; Length 1518;
Pred. No. 0.25;
0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                           911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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TITLE OF INVENTION: PAPILLOMA VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3000 K Street, N.W CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09162904A Patent No. US20020168372A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09824017
Publication No. US20020197668A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                               Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY 6
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COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-162-904A-2/c
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Gaps

TELECOMMUNICATION INFORMATION

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Search completed: March 5, 2006, 22:49:28 Job time : 362 secs
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PRIOR FILING DATE: 2002-02-14
PRIOR PILING DATE: 2002-02-14
PRIOR PLING DATE: 2002-02-14
PRIOR PAPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR PILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR PILING DATE: 2002-02-14
PRIOR PILING DATE: 2002-02-14
PRIOR PLING DATE: 2002-02-14
PRIOR PLING DATE: 2002-02-14
PRIOR PAPLICATION NUMBER: US 60/356,113
PRIOR PILING DATE: 2002-02-14
PRIOR PELING DATE: 2002-02-14
PRIOR PRESENT SOURCE SOU
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Publication No. US20030228696A1
GENERAL INFORMATION:
APPLICANT: Robin A. Robinson
TITLE OF INVENTION: No. US20030228696A1e1 Insect Cell Line
FILE REFERENCE: 44149-1US1
CURRENT APPLICATION NUMBER: US/10/367,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: CDS
; LOCATION: 1..1515
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-986-118A-1
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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                                                                                                                                                         TITLE OF INVENTION:

FILE REPERIENCE: 44149-11051

CURRENT APPLICATION NUMBER: US/10/367,095

CURRENT PERILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR PLILING DATE: 2002-02-14

PRIOR FILING DATE: 2002-02-14

PRIOR PLILING DATE: 2002-02-14

PRIOR PLILING DATE: 2002-02-14

PRIOR FILING DATE: 2002-02-14
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                                      ; Sequence 12, Application US/10367095; Publication No. US20030228696A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
US-10-367-095-12/c
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LENGTH: 1518
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911 GCATCAGAGGTAACCATAGAACCACTAGG 883

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5, 2006, 22:06:14; Search time 457 Seconds (without alignments) 139:129 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USOB NEW PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/USII_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USII_NEW_PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7218535 segs, 1096242582 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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29
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                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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		Description	Sequence 2, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 10, Appl	Sequence 12, Appl	Sequence 1, Appli	Sequence 151425,	Sequence 661735,	Sequence 661736,	Sequence 13399, A	Sequence 13400, A	Sequence 537693,	Sequence 727186,	Sequence 31766, A	Sequence 31766, A	Sequence 800, App	Sequence 800, App	Sequence 27379, A	Sequence 42693, A
SUMMARIES		ΩI	US-10-514-878A-2	US-10-514-878A-4	US-10-514-878A-6	US-10-514-878A-8	US-10-514-878A-10	US-10-514-878A-12	US-11-179-478-1	US-09-925-065A-151425	US-09-925-065A-661735	US-09-925-065A-661736	US-09-925-065A-13399	US-09-925-065A-13400	US-09-925-065A-537693	US-09-925-065A-727186	US-10-750-185-31766	US-10-750-623-31766		US-11-128-049-800	US-10-995-561-27379	US-10-995-561-42693
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		datch Length DB	1518	1518	1518	1518	1518	1518	1518	421	567	567	541	541	586	645	1021	1021	2457	2457	201	201
	Query	Match	83.4	83.4	83.4	83.4	83.4	83.4	83.4	69.7	64.8	64.8	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	61.4	61.4
		Score	24.2	24.2	24.2	24.2	24.2	24.2	24.2	20.2	18.8	18.8	18	18	18	18	18	18	18	18	17.8	17.8
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Sequence 14923, A Sequence 33222, A Sequence 689089, Sequence 689089, Sequence 13238, A	Sequence 13286, A Sequence 54678, A Sequence 35843, A Sequence 35843, A Sequence 709891,			Sequence 93734, A Sequence 103917, Sequence 301382, Sequence 301381, Sequence 301380,
12 US-11-124-367A-14923 12 US-11-124-367A-33222 S US-09-925-065A-689088 5 US-09-925-065A-689089 US-10-995-561-13238	8 US-10-995-561-13286 US-09-925-065A-54678 US-10-750-185-35843 US-10-750-623-35843 US-09-925-065A-709891	US-10-750-185-59924 US-10-750-623-59924 US-09-925-065A-796428 US-09-925-065A-851486 US-09-925-065A-796346	US-09-925-065A-851448 US-09-925-065A-274631 US-09-925-065A-411761 US-09-925-065A-411762 US-09-925-065A-391311	US-09-925-065A-99734 US-09-925-065A-103917 US-09-925-065A-301382 US-09-925-065A-301381 US-09-925-065A-301380
	1125000 814 6 1753 8 1753 8 2129 6	3045 3045 3045 449 649 654 6645	5222 5223 5255 6666	5 2 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
61.4 61.4 61.4 61.4	60.7 60.7 60.7 60.7	60.7 60.7 60.0 60.0	60.00 60.00 60.00	00000
17.8 17.8 17.8 17.8	17.8 17.6 17.6 17.6	17.6 17.6 17.4 17.4 17.4	17.4 17.4 17.4 17.4	4.71 4.71 4.71 4.71
c 21 22 23 24 25	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	31 32 34 35 35	0 0 3 3 3 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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## ALIGNMENTS

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USS-10-514-878A-2/C
Sequence 2, Application US/10514878A
Sequence 2, Application US/10514878A
Sequence 2, Application No. US2006003519A1
GENERAL IMPORMATION: University of Cape Town
TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 il Virus-Like Particles and Met
TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 il Virus-Like Particles
TITLE OF INVENTION: Perpairing the Particles
TITLE OF INVENTION: Chimaeric MANBER: US/10/514,878A
CURRENT PILING DATE: 2004-11-16
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
LEMATH: 15.18
VERBER PER SEM SEQ ID NOS: 14
SOCTHAND SEQ ID NOS: 14
SEC ID NO 2
LEMATH: 15.18
VERBER IN Human papillomavirus
US-10-514-8784-2
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Mismatche
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APPLICANT: University of Cape Town
TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
TITLE OF INVENTION: Preparing the Particles
TITLE OF INVENTION: Preparing the Particles
FILE REFERENCE: 10/514,878
CURRENT APPLICATION NUMBER: US/10/514,878A
CURRENT FILING DATE: 2004-11-16
SUFFWARE: Patentin version 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/10514878A

Sequence 12, Application US/10514878A

Publication No. US20060035319A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met TITLE OF INVENTION: Preparing the Particles
TITLE OF INVENTION: Preparing the Particles
TITLE OF INVENTION: WUMBER: US/10/514,878A

CURRENT APPLICATION NUMBER: US/10/514,878A

CURRENT FILING DATE: 2004-11-16
SOFTWARE: PatentIn version 3.1

SEQ ID NO 12

SEQ ID NO 12

SEQ ID NO 12

SEQ ID NO 12

SEQ ID NO 12
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Pred. No. 0.066;
0; Mismatches 3; Indels
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Publication No. US20050249745A1
Publication No. US20050249745A1
Publication No. US20050249745A1
Publication No. US20050249745A1
Publicant: BURGER, Michael
APPLICANT: HALLEK, Michael
TITLE OF INVENTION: PAPILLOWA VIRUS CAPSOMERE VACCINE
TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.4%; bcc. No. v.. 89.7%; Pred. No. v..
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                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human papillomavirus US-10-514-878A-12
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATING
OPERATING SYSTEM: PC-DOS/M
                                                                                                                                                                                                                                                                                                                                                               83.4%;
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 89.73
Matches 26; Conservative
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Best Local Similarity 89.73
Matches 26; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-514-878A-12/C
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US-11-179-478-1/c
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                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10514878A
Sequence 6, Application US/10514878A
Publication No. US20060035319A1
GENERAL INFORMATION:
APPLICANT: University of Cape Town
APPLICANT: University of Cape Town
TITLE OF INVENTION: Preparing the Particles
FILE REFERENCE: 10/514,878
CURRENT APPLICATION NUMBER: US/10/514,878A
CURRENT APPLICATION DATE: 2004-11-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Cape Town
TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
TITLE OF INVENTION: Preparing the Particles
TITLE REPERENCE: 10/514,878
CURRENT PELICATION NUMBER: US/10/514,878A
CURRENT FILING DATE: 2004-11-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
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                                                                                         / Match 83.4%; Score 24.2; DB 7; Length 1518; Local Similarity 89.7%; Pred. No. 0.066; les 26; Conservative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10514878A Publication No. US20060035319A1 GENERAL INFORMATION:
                      ORGANISM: Human papillomavirus US-10-514-878A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human papillomavirus
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Matches 26; Conservative
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  TYPE: DNA
                                                                                                Query Match
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Matches
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; ORGANISM: Homo sapiens
US-09-925-065A-661735
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SEQ ID NO 661736
LENGTH: 567
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 83.4%; Score 24.2; I
Best Local Similarity 89.7%; Pred. No. 0.00
Matches 26; Conservative 0; Mismatches
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PRIOR PILING DATE: 2000-10-24
PRIOR PELLING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR PELING DATE: 2001-11-30
PRIOR PELING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-05-09
PRIOR PELING DATE: 2001-05-09
PRIOR PELING DATE: 2001-05-09
PRIOR PERIOR DATE: 2001-05-09
PRIOR PELING DATE: 2001-05-09
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CURRENT FILING DATE: 2001-08-08
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Pred. No. 4
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPHONE: (202) 672-5309
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151425, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/654,129
FILING DATE: 04-Sep-2003
                                             APPLICATION NUMBER: US/11/179,478
FILING DATE: 13-JULY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 81.5%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         1518 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-09-925-065A-151425
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LENGTH: 421
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; LOCATION:
US-11-179-478-1
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                                                                      TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-16
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FOURIER INFORMATION: David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108027.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
Sequence 661735, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 GrcadadGrdaccarddaGcca 404
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Best Local Similarity 90.55
These 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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Sequence 537693, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE REFERENCE: 10827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR PELING DATE: 2000-10-24

PRIOR PELING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
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US-09-925-065A-727186/c

i Sequence 727186, Application US/09925065A

j Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,766

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/260,766

PRIOR PILING DATE: 2001-01-16
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Best Local Similarity 80.8%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 727186
LENGTH: 645
                                                                                                                                      262 TCAGAGGATGCAGTAGAGACACTAGG 287
                                                                                         4 TCAGAGGTTACCATAGAGCCACTAGG 29
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US-09-925-065A-537693
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US-09-925-065A-537693
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827,135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
FRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6
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                                                                                                                                                                                                         Sequence 13399, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                            383 GTCAGAGGTGACCATGGAGCCA 404
3 GTCAGAGGTTACCATAGAGCCA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.1%;
Best Local Similarity 80.8%;
Matches 21; Conservative
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US-09-925-065A-13399
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US-09-925-065A-13400
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LENGTH: 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: HOLM, Tom
PPLICANT: BATES, Stephen
PPLICANT: FANTIN, Dennis
ITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                               Query Match 62.1%; Score 18; DB 6; Length 645; Best Local Similarity 80.8%; Pred. No. 59; Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 31766
LENGTH: 1021
                                                                                                                                                                                                                                                                                                     Sequence 31766, Application US/10750185; Publication No. US20050260603A1; GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: RESENBELD, David
APPLICANT: ROSENBELD, David
                                                                                                                                                                              350 GCTTCAGAGCTTACRCCAGAGCCACT 325
                                                                                                                                                1 GCGTCAGAGGTTACCATAGAGCCACT 26
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; ORGANISM: Bovine 19866881678791
US-10-750-185-31766
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US-09-925-065A-727186
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US-10-750-185-31766
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Search completed: March 5, 2006, 22:37:01 Job time : 458 secs

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1 GCGTCAGAGGTTACCATAGAGCCACT 26

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Run on:

Sequence:

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DQ003071 803 bp DNA linear VRL 15-AUG-2005
Human papillomavirus type 35 nonfunctional L1 gene, partial
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Direct Submission
Submitted (08-ARR-2005) Institute of Genetics and Developmental
Biology, Chinese Academy of Sciences, AS Datun Raod, Chaoyang
District, Beijing 100101, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 803)
Mu,X., Ren,J., Ran,D. and Ma,R.Z.
Detection of HPV types in cervical brush samples of clinical
patients in Beijing and other Northern China cities
Unpublished 1 to 803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/isolation source="epithelial cells from cervix"
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Human papillomavirus type 35
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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/note="nonfunctional L1 due to mutation"
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89.0%; Score 25.8; DB 13;
Best Local Similarity 93.1%; Pred. No. 0.097;
Matches 27; Conservative 0; Mismatches 2;
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DQ003071/c
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DEFINITION
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KEYWORDS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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X74474 Human papil

X74477 Human papil

X74477 Human papil

U37488 Human papil

AR2939561 Human pap

AY098925 Human pap

AY098926 Human pap

AY098926 Human pap

AY098926 Human pap

AX70809 Sequence

AX770809 Sequence

AX770801 Sequence

AX770801 Sequence

U34165 Human papil

U34165 Human papil

U34166 Human papil

U34166 Human papil
                                                                           5, 2006, 21:52:50 ; Search time 907 Seconds (without alignments) 1817.486 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                     11766282
        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                            5883141 segs, 28421725653 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      - nucleic search, using sw model
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HPV30
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Gapop 10.0 , Gapext 1.0
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Minimum DB Maximum DB

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                                                                   product="transforming protein"
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FACYDLCIVYREGOPYGVCKKCLKFYSKISBYRWYRYSVYGETLERQCNKQLCHLLIR
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                                                                       remssows 7851 bp DNA circular VRL 10-MAY-2002 Human papillomavirus type 35 complete genome.
M74117
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                                                                                                                                                                                                                                                                                                                                                                                                           Marich, J.B., Poutsler, A.V., Rice, S.M., McGraw, K.A. and Dubensky, T.W.
The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
Virology 186 (2), 770-776 (1992)
                                                                                                                                                           complete genome; major capsid protein; minor capsid protein; regulatory protein; replication protein; transformer protein. Human papillomavirus type 35
Human papillomavirus type 35
Viruses; debnNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original source text: Human papillomavirus type 35 cervical carcinoma DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="putative; E6 ORF from bp 59 to 559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . DNA.
Location/Qualifiers
1. 7851
/organism="Human papillomavirus type 35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /proviral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17. .22
Complement (18. .26)
24. .35
Anote—"putative"
/bound moiety="E2"
/function="gene transcription"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name="Splice acceptor"
562. .861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /functTon="gene transcription"
54. .59
/note="putative"
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 799 GCATCGGAGGTTACCATAGAGCCACTAGG 771
                                                                                                                                                                                                                                                                                                                                             Virology 159, 187-190 (1991)
87265470
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'bound moiety="E2"
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/gene="E6"
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/gene="E6"
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protein_bind
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                                                                                                              DEFINITION
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                                                        RESULT 2
PPH35CG/c
                                                                                                                                ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
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CDS

gene

CDS

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KQPQQARQEEQHPCYLINTQCCRCASAVQLAVQSPTKELRALQQMLMGALELVCPLCA
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KHNCLVLYGPPNTGKSCFAMSLIQFFQGSVISYNSHSHFWLQPLDDATD
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VCREGVKRRI I DTDVADSGYGNTLEVEATQQVQDNTYGSGKQQDGGSQTSVCSRENSI
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                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (06-AUG-1993) H. Delius, Deutsches
Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506, W
6900 Heidelberg, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MASPEGTDDEGGGCTGWFHVEAVVKKRTGDIISEDETEEL"
                        gene; early protein; Ll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRCYRCOOPLTPEEKOLHCEYKKRFHRISRTWTGLCLOCWRHTTSTETAV"
                                                                                                                                                                                                    Primer-directed sequencing of human papillomavirus types Curr. Top. Microbiol. Immunol. 186, 13-31 (1994) 8205838
X74474.1 GI:396973
BI gene; E2 gene; E4 gene; E7 gene; early protest gene; L2 gene; Late protein.
Human papillomavirus type 30
Human papillomavirus type 30
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Human papillomavirus type 30"
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(db_xref="UniProt/Swiss-Prot:P36826"
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db_xref="GI:396976"
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product="early protein"
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protein_id="CAA52544.1"
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product="early protein"
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                                                                                                                                                                    1 (bases 1 to 7852)
Delius, H. and Hofman
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/gene="E6"
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/gene="E6"
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/gene="E7"
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/gene="E1"
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/gene="E7"
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                                                                                                ORGANISM
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AUTHORS
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PUBMED
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JOURNAL
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  VERSION
KEYWORDS
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                                                                                                                                                                                                                     TITLE
                                                                   SOURCE
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ELQPLQHVPSSLPHTTVSTSLNDGMFDIYAPIDTEEDIIFSASSNNTLYTTSNTAYVP
SNTTIPLSSGYDIPITAGPDIVFNSNTITNSVLPVPTGPIYSIIADGGDFYLHPSYYL
                                                                                                                                                                                       1LKYGSMAVFFGGLGIGSGSGTGGRSGYVPLGTTPPTAATNIPIRPPVTVESIPLDTT
GPLDSSIVSLVETVSFIESGAPVVTPRVPPTTGFTITTSTDTTPAILDVTSISTHDNP
                                                                                                                                                                                                                                       TPTDPSVLHPPTPAETSGHFVLSSSSISTHNYEEIPMDTFIVSTDSNNITNSTPIPGS
                                                                                                                                                                                                                                                                  RPTTRLGLYSKGTQQVKVVDPAFMTSPAKLITYDNPAYEGLNPDTTLQFEHEDISLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGCRPPIGEHWGKGTPCNANQVKAGECPPLELLNTVLQDGDMVDTGFGAMDFTTLQA
NKSDVPLDICSSICKYPDYLKMVSEPYGDMLFPYLRREQMFVRHLFNRAGTVGETVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDTTRSTIMMSVCSAVSSBOSTYKNDNFKEYLEHGEEVDLOFIFOLCKTTLTADVMTYI
HSMNPSILEDWNFGLTPPPSGTLEDTYRYVTSQAVTCQKPSAPKPKDDPLKNYTFWEV
DLKEKFSADLDQFPLGRKFLLQAGLKARPNFRLGRRAAPASTSKKSSTKRRKVKS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'translation="MSLWRSNEATVYLPPVSVSKVVSTDBYVTRTNIYYHAGSSRLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGHPYYA I KKQDSNK I AVPKVSGLQYRVFRVKLPDPNKFGFPDTSFYDPCLQRLVWAC
IGVEVGRGQPLGVG I SGHPLLNKLDDTENLNKYVGNSGNSGTDNREC I SMDYKQTQLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLY I KGTTGTLPSTSYFPTPSGSMVTSDAQI FNKPYWLQRAQGHNNGI CWSNQLFVTV
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7477. .7491
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complement(7670, .7677)
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(K.Coctomer)"
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Pred. No. 0.086;
0; Mismatches 2;
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Human papillomavirus type 30 genomic DNA.
X74474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                                                 'note="putative; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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7695. .7700
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534. 7539
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db_xref="G1:333058
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'bound_moiety="E2"
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Best Local Similarity 93.1
Matches 27; Conservative
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repeat_region
protein_bind
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enhancer

ACWRYIDEYMRNLLDGNPVSLDRKHKQLVQIKCPPVIITTNINPLHDAKLQYLHSRIH

の名話がつい

LOCUS DEFINITION ACCESSION

RESULT 3 HPV30/c

ઠે 원 VRL 18-APR-2005

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**JVPFLNPFPIDTNGNPVYQLNNVNWKCFFERTWSRLDLNNDEDKENHGDSMPTFRCVP** 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-AUG-1993) H. Delius, Deutsches
Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506,
6900 Heidelberg, FRG
                                                                                                                                                                                                                    El gene; E2 gene; E4 gene; E6 gene; E7 gene; early protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delius, H. and Hofmann, B. Primer-directed sequencing of human papillomavirus types Curr. Top. Microbiol. Immunol. 186, 13-31 (1994) 8205831
                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Human papillomavirus type 35H"
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                                                                      linear
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Human papillomavirus type 35H genomic DNA.
X74477
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Human papillomavirus type 35H
Human papillomavirus type 35H
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/gene="E1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDGNKVYYTDFNDEAVKYGYKGTWEVHMGNES IYCPDSVSSTLRSNVSPVETVVEYNT
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TYGOLI IGCTPAI GERWAKGTACRSAPPAĞGDCPELELVWST DYOGWNDIGFGAMDFK
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4280. .5671
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Gaps ö

Indels

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0; Mismatches

Conservative

Ouery Match Best Local Similarity Matches 27; Conserv 27;

ORIGIN

Length 7852;

89.0%; Score 25.8; DB 13; 93.1%; Pred. No. 0.086;

6562

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1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29

VRL 06-DEC-1999

linear

54 54

to 7759)

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Direct Submission
Submitted (03-OCT-1995) Andrew Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501 USA
HPV-54 was first isolated from a patient with condyloma acuminata.
Location/Qualifiers
1,7759
                                                                                                                                                                                                                                                                         Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 7759)
nruj7488 7759 bp DNA line
Human papillomavirus type 54, complete genome.
U37488
                                                                                                                                                                                            Human papillomavirus -
                                                                                                                            U37488.1 GI:1017782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  armer, A.D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
2 (bases 1
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        LOCUS
DEFINITION
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KEYWORDS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="early
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note="putative; ORF E7 from bp 512 to 823"

gene="E7" gene="E7"

note="putative; ORF E6 from bp 7708 to 536"

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102. .536 /gene="E6" 102. .536 /gene="E6"

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QTVSGSTTTDSLGRQQTBLIHNTNIRVALGEMFKDLYGLSFMDLARPFKSDKTVCTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVIAARGIYHGITDGFKTLLEPHCLYGHIQWLTCRWGMVLLLLTRFKCGKNRLTVSKC
LGMLLNIPETQMLIDPPKLRTPAAALYWYRQGLSNASEIRGTPPEWLARQTVIEYSLA
DSQFDLSKWYQWAYDHNYIDDSIIALEYAKLADIDENAAAFLGSNCQAKYVKDCGTMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKHNCI LLYGPDTGKSNFAMSLI SFLGGVVLSYVNSSSHFWLEPLADAKIAMLDDAT
TQCWNYMDI YMRNALDGNPMCFDRKHRAMVQTKCPPLI VTSNI NASTDDRWRYLHSRV
KCFCFPNRPPFDSNGNPVYDLSNKNWKSFFKRSWSRLALNDNDNEEEENGDPSNTFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHYI RAQKWQWTMSQWI KHRCDLVEBEGEWKEI VRFLRYQHVDFI SFMI ALKQFLQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2671. .3774
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                                                                                                                                                                                                                   828. .2729
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                                                                                                                                                            828. .2729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6505 GCATCGGAGGTTACCATAGAGCCACTAGG 6477
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SCO

RESULT 5 HPU37488/c

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codon_start=1
                  GI:13507120
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                                                                                                                                                     (bases 1 to 7904)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .456
/gene="E6"
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                    AF293961.1
AF293961
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                                                           SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                            AUTHORS
TITLE
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AUTHORS
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ACCESSION
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                      VERSION
KEYWORDS
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                                                                                                                                                   YMDAEHKVYYVDFKKEASKYGEŸGQWEVRMGSSIIFSPASVSSTEEALSISSTGTAEH
TRABANETPETTDNSTKALPTCPPPRKRARVYSTDOQPHGTSDPVGCDNDRHISDDNNKN
QGRHTSSGDTTPIVHEKGEPNTLKCFRQRIQKYKHLFEQASSTWHWACVPGTTKNRGI
VTLTYSSVEQRQQFLVTVRIPPSISMSLGVWSL"
                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="momvfilwmontkcimmilkrkhlsmgnmdsgrcvmaaasffll
hlylvpkrhcompliallntpdoppiphhvpttpokosrarrienelestaotsnhta
potpwavyttgtsvtittrtkdgtovvvtlhl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYTEPSLLIDPPPVQWIGGRULVSTSTLQSSTAENIPMDTFIIMQDHIGTTTSTPIPRP
PARRELGYSKALQQVPVQDPAFLQQPSSLITYDNPVYEGNPDVTLHEEQPTHNAPD
PARMDIFALHREALTTRRGVVRYSRVORDRATLHTRSCLQLKRRVHFRQDLSPIAHVPE
EIEHPLISANNTSINNGLYSDIYDVYADTDPADTGESSSTVSHSSVQTALQTTSIP
SQYGNTTVPLTASSPYTPIPTSFRPSSGHTPFVPARPIFPQTPIAVNGGDFYLHPSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mwrpsenkvylpptpvskvvstdevvtrtsiyyhasssrllavg
hpypkvoktwnkosipkvsgyqyrvfrvolpdpnkfglpdpslynpetqrlgv
evgrgqplglglglsghpllnklddtenapkyvgagadnrenvsmdykqTqlcilgctpp
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SGNLDSSIYAATPSGSMYTSEYQIFNKFYMLQRAQGQNNGICMGNQYELTVVDTTRST
NLTLCATASTQDSFNNSDFREYIRHVEEYDLOFIFQLCTITLTADVMAYIHGMNPTIL
EDWNFGITPPATSSLEDTYRFWGQAALACQKNNAPAKEKEDPYSKFNFWTVDLKERFS
SDLDQFPLGRKFLLQAGLRARPRLRPVKRAAPSSSKGTARKRAKTKR"
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                                                                                                         KAREMGYKVLQHQALPALAVSKGKGHKAIELQLALETLQKTVYSTEPWTLQDTCLERW
NAPPTGCLKRRGQTVDVIPDGHQDNTMQYVMWGDIYYQNCDGEGWTKVCSNIDAMGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRWGSMGVFFGGLGIGTGSGTGGRTGYIPLGRPSTTLEPGPPVRPAGAVETVAPSDPS
IVSLVEESSVVDVGAPTPTIPSQGGFEIATSSDATPAILDVTSTTTPIRVSITSHDNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEHWAKGNLCTPNTLAAGDCPPLELVNSYIQDGDMVDIGFGAMDFKTLQTSKSEVPL
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Human papillomavirus type 82 subtype IS39/AE2, complete genome.
                                                                                    translation="METLATRLDVCQERLLDLYEKDSNKLEDQIEHWKCIRLECALQY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MAKARAPRRKRASATQLYQTCKASGTCPSDVIPKVEGTTIADQL"
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                                                                                                                                                                                                                                                                                                                                 note="putative; ORF E4 from bp 3134 to 3538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="putative; ORF L2 from bp 4200 to 5627"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="putative; ORF L1 from bp 5422 to 7107" (codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="major capsid protein"
protein id="AAA79193.1"
db_xref="G1:1017789"
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/db_xref="GI:1017788"
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5614. .7107
/gene="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4215. .5627
/gene="L2"
4215. .5627
/gene="L2"
                                                                                                                                                                                                                                          3134. .3538
/gene="E4"
                                                                                                                                                                                                                                                                                     3<u>1</u>34. .3538
/gene="E4"
                                                                                                                                                                                                                                                                                                                                                        /codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'codon
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Matches 25; Conserv
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AF293961/c
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DEFINITION
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Handbern Papillomavitus type 82

When papillo
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gene

CDS

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624 bp DNA linear VRL 26-MAY-2002
Human papillomavirus type 16 isolate Bsb-102 major capsid protein
AY098925
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/product="major capsid protein L1"
/protein_id="hajor capsid protein L1"
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RFVTQAIACQKHTPPAPKEDDPLKKYTFWEVNLKEKFSADLDQFFLGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        635 bp DNA linear VRL 26-MAY-2002
Human papillomavirus type 16 isolate Bsb-178 major capsid protein
AY098921
                                                                                                                                                                                                                                                                                                                                                                                                Cruz, M.R. and Marrins, C.R.F.
Direct Submission
Submitted (23-APR-2002) Cellular Biology, UnB, Campus UnB,
Brasilia, DF 70.910-900, Brazil
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                     Viruses, dsDNA viruses, no RNA stage, Papillomaviridae,
Alphapapillomavirus
1 (bases 1 to 624)
                                                                                                                                                                                                                                                                                     Cruz.M.R., Cerqueira,D.M., Camara,G.N.L., Silva,E.O.,
Carvalho,L.G.S. and Martins,C.R.F.
Human papillomavirus type 16 variants in Central Brazil
Unpublished
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Human papillomavirus type 16
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24.2; DB 13; Length
Pred. No. 0.64;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .624
/organism="Human papillomavirus type 16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/isolate="Bsb-102, European"
/db_xref="taxon:333760"
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                                                                                                                                                                         Human papillomavirus type 16
Human papillomavirus type 16
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89.7%; Pred
0; h
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<1. .>624
/gene="L1"
                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 624)
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Best Local Si
Matches 26;
RESULT 7
AY098925/c
LOCUS
DEFINITION
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VERSION
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SOURCE
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LOCUS
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                                                            PDVHKEYYVKFIEEAKKYGAQQMEVYMCGNVITCPEYVSSTCRDPLFSTTTVEQHSNT
TYTNYTTYSVOTKRAQAPQQRKAQRITBEDSSTVTPLSVDTCHQIHCGTGSANTGGH
QSATKTAFIVHLKGATNCLKCLRYRESKHRNLFKEVSSTWHWTSNTKAGIVTITFDSA
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3788. 4036
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GVRRIAAPRLYSKAFTQVKVTNPDFISRPSSFVTFDNPAFEPIDASLSFGEFTTVAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDFLDIIKLHRPALTSRRGTVRFSRLGQKATIRTRSGKQIGAVHYYHDISNITPTEE
LEMQPLLSBSTNNYSYDIYADLDEAETGFIQPTHTTPMLRSSYSPLSTQLPSLSSSVS
SSYANVTIPPSTTYHVPIHTGPDVVLPTSPTWPPIPHTSIDTQHAIVIQGGDYYLWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative major capsid protein L1"
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/db xref="cd:13507128"
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GVBVGRGQPLGVGLSGHPLFNKYDDTENSRVANGNVQQDVRDNISVDNKQTQLCIIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPIGEHWATGTTCKNVPVPQGDCPPLELVSTIIBDGDMIDTGFGAMDFANLQATKSD
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KGTGTGRDPIGSYI YSATPSGSMVTSDSQI FNKPYMLHRAQGHNNGI CWNNQLFITCV
DTTRSTNLTI STAATPSVAQTFTPTNFKQY I RHGEEYELQFI FQLCKI TLTTEVMAYL
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DLKERFSLDLDQLALGRKFLLQIGAQRKARPGLKRPAPSSSSSSSSKRKRVKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'codon_start=1
'product="putative minor capsid protein L2"
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'db_xref="GI:13507127"
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'codon_start=1
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                                                                                                                                                                                                                                                                     product="putative
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                                                                                                                                                                                                                                                codon_start=1
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4068. .5489
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Best Local Similarity
Matches 25; Conserv
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gene

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CDS

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Gaps

Human papillomavirus type 16 variants in Central Brazil Unpublished
2 (bases 1 to 635)
Cruz, M.R. and Martins, C.R.F.
Direct Submission

TITLE JOURNAL REFERENCE AUTHORS TITLE

6377 TCAGAGGTTACCATAGAGCCACTTGG 6352 4 TCAGAGGTTACCATAGAGCCACTAGG 29.

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The william was

us-10-720-424b-8.rge

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/dx xxef="c1:6686321"
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PSPGDSLPFFTLRRQMYFWLHDRAAANGBNVPDDLYIKGSGSTANLASSNYFPTPSG
SMYTSDAQIPKPPYALQRAQGHVDGICWGNOLFVTVVDTTRSTNASLCAAISTSETTY
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YKNTNFKEYLRHGEBYDLQFIFQLCKITLTADVMTYIHSMNSTILEDMNFGLQPPPGG
TLEDTYRFVTQAIACQKHTPPAPKEDDPLKKYTFWEVNLKEKFSADLDQFPLGRKFLL
QAG"
                                                                                                                                                                                                                                                                                                      VRL 15-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu, X., Ren, J. and Ma, R.Z.
Direct Submission
Submitted (08-APR-2005) Institute of Genetics and Developmental
Biology, Chinaes Academy of Sciences, A5 Datun Raod, Chaoyang
District, Beijing 100101, China
Location/Qualifiers
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Detection of HPV types in cervical brush samples of clinical patients in Beijing and other Northern China cities
Unpublished
2 (bases 1 to 799)
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/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolation_source="epithelial cells from cervix"
/sub_species="16"
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Human papillomavirus type 16
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
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gene, partial cds.
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89.7%; Pred. No. 0.63;
iive 0; Mismatches 3;
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                                                                                             Score 24.2; DB Pred. No. 0.64;
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Human papillomavirus type 16 L1
AF512011
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Human papillomavirus type 16
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                                                                                                                                                                                                                                                                                                                                                             GI:66866320
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                                                                                               83.4%;
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DQ003067/c
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DTYRFVTQAIACQKHTPPAAFKEDDPLKKYTFWEVNLKEKFSADLDQFPLGR"
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2 (bases 1 to 667)
2 (Laz.M.R. and Martins,C.R.F.
Ciraz.M.R. and Martins,C.R.F.
Direct Submission
Submitted (21-APR-2002) Cellular Biology, UnB, Campus UnB,
Brasilia, DF 70.910-900, Brazil
Location/Qualifiers
Submitted (23-APR-2002) Cellular Biology, UnB, Campus UnB,
Brasilia, DF 70.910-900, Brazil
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; deDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.

1 (bases 1 to 667)

Cruz,M.R., Cerqueira,D.M., Camara,G.N.L., Silva,E.O., Carvalho,L.G.S. and Martins,C.R.F.

Human papillomavirus type 16 variants in Central Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 635;
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                                                                      /organism="Human papillomavirus type 16"
/virion
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                                                                                                                 /mol_type="genomic DNA"
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/db_xref="taxon:333760"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.4%; Score 24.2; DB 13; Best Local Similarity 89.7%; Pred. No. 0.64; Matches 26; Conservative 0; Mismatches 3;
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/note="genotype: 16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 GCATCAGAGGTAACCATAGAACCACTAGG 119
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                                                                                                                                                                       /note="genotype: 16"
<1. .>635
/gene="L1"
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Human papillomavirus type 16
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/gene="L1"
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                                                                                                                                                                                                                                                                     codon_start=2
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**Gaps** 

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PAT 02-JUL-2003

ORGANISM

AUTHORS TITLE

REFERENCE

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

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Varsani, A.D., Rybicki, E.P. and Williamson, A.L.
Pharmaceutical compositions, and a method of preparing and
isolating said pharmaceutical compositions, and use of said
pharmaceutical compositions for prophylactic treatment of lesions
                                                                                                                                                                                                                                                                                                                                                 RNA stage; Papillomaviridae;
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   Length 1452;
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Lorincz,A.T. and Lazar,J.G.
Assessment of human papillomavirus-related disease
Patent: US 6355424-A 2 12-MAR-2002;
                                                                                                                                                                                                                  linear
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   83.4%; Score 24.2; DB
89.7%; Pred. No. 0.61;
iive 0; Mismatches
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Patent: WO 03018623-A 4 06-MAR-2003;
University of Cape Town (ZA)
Location/Qualifiers
                                                                                                   911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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                                                                                                                                                                                                    AX770811 1452 bp
Sequence 4 from Patent WO03018623.
AX770811
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                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA unclassified Papillomaviridae.
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89.7%; Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Ll protein"
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EEYDLQEIPQLCKITLTADVTTYIHSM"
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AANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCTNVAVNPGDCPPLELINT
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bharmaceutical compositions, and a method of preparing and isolating said pharmaceutical compositions, and use of said pharmaceutical compositions for prophylactic treatment of lesions
                                                                                         Cloning and sequence analysis of Human papillomavirus type 16 Ll gene in China Unpublished
2 (bases 1 to 1257)
Zhang, J. and Chen, R. Briect Submission
Submitted (L-MAY-2002) Fourth Military Medical University, Institute of Gene Diagnosis, Changle West Road 17, Xian, Shaanxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Human papillomavirus type 16
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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89.7%; Pred. No. 0.62;
ive 0; Mismatches 3;
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University of Cape Town (ZA)
Location/Qualifiers
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1 (bases 1 to 1257)

Zhang, J. and Chen, R.
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AX770809/c
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PAT 20-APR-2002

DEFINITION ACCESSION

SOURCE ORGANISM

VERSION KEYWORDS

REFERENCE AUTHORS TITLE

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FEATURES

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Human papillomavirus type 16, isolate NM 4094, late major capsid protein L1 (L1) gene, partial cds.
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Submitted (17-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
Location/Qualifiers
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RESULT 15
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Gaps ö 83.4%; Score 24.2; DB 13; Length 1484; 89.7%; Pred. No. 0.61; Indels 3, 0; Mismatches Best Local Similarity 89.79 Matches 26, Conservative Query Match

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ð 셤 Search completed: March 5, 2006, 22:23:15 Job time : 908 secs

Aag39483 PCR Prime Abk40943 Human obe Ads90978 Oligonucl Aea80760 Human tum

Abk57201 Abk56012

Aas94223 PCR prime Aas42900 Human G P Adp68078 Human jag Adp68043 Human jag

Aav32488 Human ret Aar55850 Human ret Adn35455 Human mic Ac149246 Human mic Ac15509 Human mic Ac16394 Human mic Ac28706 Human mic Ac87706 Human mic Ac87708 DNA probe Adw01878 DNA probe

Human alc Human alc

Abk86296 B Abz43753 B Abz49321 B Aaz67316 B Aas42897 B

Human Human Human

Perfect score:

Sequence:

World-size-

Searched:

Database :

OM nucleic

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New general primer or primer pair, useful for amplifying and detecting, or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
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Human Papillomavirus genotype; cervical-neoplasia;
oncogenic high-risk group.
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ACI49246
ACK15509
ACI16394
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                             AAQ39483
ABK40943
ADS90978
AEA80760
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ADW01878
ABK86296
ABZ43753
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AAZ67316
AAS42897
AAI77901
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31-JUL-2003; 2003KR-00053147.
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Aac23878 Human pap
Abf76716 Oligonucl
Abf76717 Oligonucl
Abk56011 Human CLC
Abk57423 Human CLC
Aag61872 DNA captu
Aav07712 HPV-18 pr
Ad078152 Human CLC
Adu26858 Knock-dow
Adq77975 Human pap
Abr84687 HIV-1 amp
Abr84680084 Human ALD
Abr84000844 Nicotiana
Ad900344 Nicotiana
Adb94574 Gene prom
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                                                               5, 2006, 22:08:34 ; Search time 271.5 Seconds (without alignments) 711.882 Million cell updates/sec
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          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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ABK56011
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Match Length
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                                                                   March
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The invention relates to a general primer or primer pair for amplifying and detecting or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes. The general primers are useful for amplifying cervical-neoplasia related HPV genotypes including

ADG00344 ADH94574

Score

Result Š. U

Claim 1; SEQ ID NO 4; 71pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acids to at least two or more nucleic acid probes are attached to a solid support. The analysis comprises monitoring pene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acid further comprises a tag sequence. The array of nucleic acid
oncogenic high-risk groups and low-risk groups. The general primers are useful for producing amplifying products to DNA of scores of diverse oncogenic HPV types and thus detecting the oncogenic HPV types in a sample but also to select cervical carcinoma and its pre-stage lesions at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes is useful in a situ hybridisation, in Southern, Northern or dot-
blot hybridisation to identify or detect the sequence or specific
mutations of any gene, in mapping the 5' termini of mRNA molecules by
primer extensions or in screening CDNA or genomic libraries or subclones
for additional subclones containing segments of DNA that have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                            early stage by improving sensitivity according to HPV types. This sequence corresponds to PCR primer used in the invention.
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                          100.0%; Score 29; DB 12; Length 29; 100.0%; Pred. No. 1.3e-06;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human microarray DNA oligonucleotide SEQ ID NO 16386.
                                                                                                                                                  Sequence 29 BP; 8 A; 1 C; 11 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                              1 Similarity 100.0%; Pred. No. 1.3
29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                  1 GATGGTGATATGGTAGATACAGGATTTGG 29
                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 16386; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ACI16395 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LS-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-567953/53.
                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACI16395;
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
ACI16395/c
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isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compsns. for amplifying DNA of human papilloma virus by LCR and PCR - consensus and type specific oligo-nucleotide(s), for diagnosis of HPV-esp. types 6,11,16,18 33 and 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                             Gaps
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                                                                                                             Length 25;
                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consensus regions with homology among different types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18 + Example 5; Page 69 + 11-13; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38 BP; 8 A; 3 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  Human papilloma virus; LCR; ligase chain reaction;
                                                                          Sequence 25 BP; 7 A; 7 C; 1 G; 10 T; 0 U; 0 Other;
                                                                                                            DB 9; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laffler TG;
                                                                                                                      100.0%; Prec. ....
                                                                                                             Score 14;
Pred. No.
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                                                                                                                                                                                                                                                                                         BP.
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                                                                                                             48.38;
                                                                                                                                                                                                                                                                                         AAQ23183 standard; DNA; 38
                                                                                                                                                                                                         25 ATGGTAGATACAGG 12
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                                                                                                                                                                           10 ATGGTAGATACAGG 23
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                           Local Similarity 100.
hes 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-106365/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                      HPV probe 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                     06-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Joseph JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP477972-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                        AAQ23183;
                                                                                                             Query Match
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                                                                                                                                           Matches
                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                          AAQ23183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                     pximer; probe; human papillomvirus; PCR; amplification; LCR; ligation;
fluorescein; biotin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human papilloma virus type-specific oligo:nucleotide(s) - used for the detection of and determination of the type of HPV in test samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide SEQ ID NO 176713 for detecting SNP TSC0043853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14; DB 2; Length 38;
Pred. No. 3.6e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 38 BP; 8 A; 3 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                Joseph JL;
                                                                                                              Human papillomavirus detection probe 36.
                                                                                                                                                                                                                                                                                                                                                                                             Laffler TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Col 13-14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.3%; Scc.
100.0%; Pred
0; M
               AAT29878 standard; DNA; 38 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                          90US-00590105.
90US-00590253.
92US-00965665.
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                                                                                                                                                                                                                                                                                               90US-00589948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATGGTGATATGGT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATGGTGATATGGT 14
                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Marshall RL, Bouma SR,
                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-087060/09.
                                                                                                                                                                                                                                                                                                                                                                   (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                            28-SEP-1990;
28-SEP-1990;
22-OCT-1992;
                                                                                                                                                                                                                                                                   30-SEP-1994;
                                                                     25-MAR-2003
19-JUL-1996
                                                                                                                                                                                                              US5484699-A.
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                                                                                                                                                                                                                                        16-JAN-1996
                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP76716;
                                           AAT29878;
AAT29878
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide SEQ ID NO 176714 for detecting SNP TSC0043853
                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 176713; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.8%; Score 13; DB 5; Length 13; 100.0%; Pred. No. 1.3e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                          Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABF76717 standard; DNA; 13 BP
                                                                                                                    06-APR-2001; 2001WO-IB000713.
                                                                                                                                                    07-APR-2000; 2000DE-01019173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GGTGATATGGTAG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGATATGGTAG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
1es 13; Conservative
                                                                                                                                                                                                                        Olek A, Piepenbrock C,
                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                       WPI; 2001-657177/75.
                                                  WO200177384-A2.
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                 Homo sapiens.
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                                                                                  18-OCT-2001
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ABF76717/c
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The invention relates to enzymatic nucleic acid molecules that down captalate expression of chloride channel calcium activated 1 (CLCA1) genes consider a paramaceutical agents. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic cobstructive pulmonary disease (OPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions contracted to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, chence, are useful for treatment of a patient having a condition contracted with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to camine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antinflamatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to enzymatic nucleic acid molecules that down
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 6 A; 2 C; 5 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ayers D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13; DB 6; I
Pred. No. 1.3e+03;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CLCA1 gene enzymatic nucleic acid #2111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mckenzie T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 134; 152pp; English.
Claim 4; Page 59; 152pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK57740 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 76.9 Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ATGGTAGATACAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 Augguagauacag 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK57740
%X55555555555555555555555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99999 and ABI00010-ABI82073 targement the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                       set or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Szymkowski DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó;
                                                                                                                                                                                           Claim 1; SEQ ID NO 176714; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.8%; Score 13; DB 5; Length 13; 100.0%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mckenzie T, Ayers D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CLCA1 gene enzymatic nucleic acid #382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was obtained in electronic format from Wi
ftp.wipo.int/pub/published_pct_sequences
Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK56011 standard; RNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001; 2001WO-US024970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2000; 2000US-0224383P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thompson J, Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GGTGATATGGTAG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGATATGGTAG 1
Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNTEX USA LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-217145/27.
                                             WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200211674-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acetylcysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK56011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Szymkowski DE;

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Length 17; 0; Indels

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regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as phramaceutical agents for treating conditions such as chronic obstructive pulmonary disease (CCDP), chronic bronchitis, asthma, cystic that are related to or will respond to the levels of CLCA1 in a cell or issue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition casciated with the level of CLCA1, where the invention further comprises the use of one or more therapy under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, and and mutations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the example of CLCA1 RNA in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 6 A; 1 C; 6 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzymatic nucleic acid molecule of the invention
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44.8%; Score 13; DB 6; Length 17; 76.9%; Pred. No. 1 3ein. 0, Indels Pred. No. 1.3e+03; 3; Mismatches 0; 10 ATGGTAGATACAG 22 |:||:||:|||| 3 AUGGUAGAUACAG 15 Local Similarity 76.9 Query Match Matches

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ABK57423 standard; RNA; 17 BP ABK57423; ABK57423 RESULT

(first entry) 02-JUL-2002 

Human CLCAl gene enzymatic nucleic acid #1794.

Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; CODD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine

Homo sapiens

WO200211674-A2..

14-FEB-2002

09-AUG-2001; 2001WO-US024970.

09-AUG-2000; 2000US-0224383P.

(RIBO-) RIBOZYME PHARM INC. (SYNT ) SYNTEX USA LLC. (THOM/) THOMPSON J.

Thompson J, Mcswiggen J, Mckenzie T, Ayers D,

Grupe A;

Szymkowski DE;

channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma. Enzymatic polynucleotide that down regulates expression of chloride WPI; 2002-217145/27.

Claim 4; Page 113; 152pp; English.

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic

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0; Gaps

1 GATGGTGATATGG 13

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Matches

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obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLGA1 in a cell or tissue. The sequences are useful for reducing CLGA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as disgnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The capture oligonucleotide AAQ61872 has unique specificity for the HPV-18 genome and is complementary to the region around nucleotide 6779 of HPV-18. The capture probe is immobilised for use in a sandwich hybridisation assay. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New conjugate for bio:luminescent hybridisation or immunoassay - comprises kinase or dehydrogenase coupled to specific ligand for the analyte, partic. for detecting human papilloma virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papilloma virus; HPV; detection; assay; cervical cancer; nucleic acid hybridisation; capture probe; sandwich assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA capture probe for detection of HPV-18 by sandwich assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zammatteo
                                                                                                                                                                                                                                                                                                                              / Match 44.8%; Score 13; DB 6; Length 17; Local Similarity 76.9%; Pred. No. 1.3e+03; Nes 10; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 44.8%; Score 13; DB 2; Length 21; Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      Sequence 17 BP; 6 A; 1 C; 5 G; 0 T; 5 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2B; Page 23; 43pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ61872 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              10 ATGGTAGATACAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AUGGUAGAUACAG 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LAMB-) LAMBDATECH SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-118481/14.
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25-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                Query Match
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The invention relates to a method for detecting and/or quantifying a target nucleotide sequence in a biological sample. It comprises contacting the sample with an immobilised capture probe and a labelled detection probe. The capture probe is a single-stranded oligonucleotide that is complementary to part of the target sequence and is covalently coupled at one end to a solid support. The detection probe is covalently complementary to another part of the target sequence. The capture probe has a length of 50-500 bases, and a portion of the capture probe that does not hybridise with the target sequence. Use of long, highly complementary capture probes improves specificity and sensitivity. The
                                                                                                                                                                                            cytomegalovirus; detection; quantifying; target nucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sandwich-type nucleic acid hybridisation assay - using long, highly complementary capture probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents a human papillomavirus (HPV)-18 primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.8%; Score 13; DB 2; Length 21; 100.0%; Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Ernest I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 5 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 43; 77pp; French.
                                                                                                                                                                                                         capture probe; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В.
                                                                                 AAV07712 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CLCAl RT-PCR primer #1.
                                                                                                                                                                                                                                                                                                                               97WO-BE000102
                                                                                                                                                                                                                                                                                                                                                          96BE-00000755.
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                                                                                                                                      25-NOV-1998 (first entry)
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               21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100
GATGGTGATATGG
                                                                                                                                                                                                                                    Synthetic.
Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-207411/18.
                                                                                                                                                                                                                                                                                                                                                                                                  (REMA/) REMACLE J.
                                                                                                                                                               HPV-18 primer
                                                                                                                                                                                                                                                                                                                                  09-SEP-1997;
                                                                                                                                                                                             HPV-18; CMV;
                                                                                                                                                                                                                                                                            WO9811253-A2
                                                                                                                                                                                                                                                                                                                                                          09-SEP-1996;
20-MAR-1997;
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                                                                                                                                                                                                                                                                                                       19-MAR-1998
                                                                                                             AAV07712;
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Matches
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                                                       RESULT 11
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The invention relates to pharmaceutical compositions that comprise an agent that inhibits the expression or activity of a tumour-associated antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAG, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAG, or related nucleic acid, antibodies or host cells, are also useful for diagnosis and monitoring of tumours. The present sequence represents a human CLCA1 reverse transcriptase (RT)-PCR primer.
ss; reverse transcriptase; RT-PCR; primer; tumour-associated antigen; TAg; cancer; lung cancer; breast cancer; prostette cancer; colon cancer; stomach cancer; pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human;
                                                                                                                                                                                                                                                                                                                                                      Composition containing inhibitor of expression or activity of specific tumor-associated antigens, useful for treating cancers, also related compositions for diagnosis and monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; RNA production; protein production; drug development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 8 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; SEQ ID NO 67; 124pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Knock-down target sequence #256.
                                                                                                                                                                                                                                                                                               Koslowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                               22-NOV-2002; 2002DE-01054601.
                                                                                                                                                                                                                               22-NOV-2002; 2002DE-01054601,
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                                                                                                                                                                                                                                                               (GANY-) GANYMED PHARM
                                                                                                                                                                                                                                                                                             Tuereci O, Sahin U,
                                                                                                                                                                                                                                                                                                                         WPI; 2004-421820/40.
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                 DE10254601-A1.
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                                                                                                   Homo sapiens.
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                                                                   CLCA1.
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(GALA-) (VSCH/)

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oncogenic HPV types and thus detecting the oncogenic HPV types in a sample but also to select cervical carcinoma and its pre-stage lesions at early stage by improving sensitivity according to HPV types. This sequence corresponds to PCR primer used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of amplification primer QAL48. This is one of a set of claimed amplification and detector primers and probes (see ABN84687-723) derived from the HIV-1 polymerase (pol) gene, which facilitate the detection and/or quantification of all presently known spencypes of HIV-1 (A-I and O). These primers and probes can be used in a variety of amplification and non-amplification formats for the detection of HIV nucleic acids. The present primer contains a 3 target binding sequence. The remaining 5' portion of the primer comprises a restriction amplification (SDA) reaction of the primer comprises a restriction amplification (SDA) reaction to proceed, and a generic non-target-specific tail sequence. The 'L' in the primer may alternatively be used as a hybridisation probe for direct detection of HIV-1, either without prior amplification or as a post-amplification assay. The primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide useful for detecting multiple human immunodeficiency virus-1 genotypes, has sequence consisting of target binding sequence and optionally, a sequence for selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV-1; detection; primer; strand displacement amplification; SDA; polymerase; enzyme; pol gene; sg.
                                                                                                                                                   44.8%; Score 13; DB 12; Length 24; ilarity 100.0%; Pred. No. 1.3e+03;. Conservative 0; Mismatches 0; Indels
                                                                                                               Sequence 24 BP; 6 A; 2 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/bound_moiety= "HIV-1 pol gene"
/note= "target binding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-1 amplification primer QAL48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 3; 16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BECT ) BECTON DICKINSON & CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-2001; 2001EP-00129200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JAN-2001; 2001US-00757207.
                                                                                                                                                                                                                                                                                                                                                                                                  ABN84687 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                            17 ATACAGGATTTGG 29
                                                                                                                                                                                                                                                                                     12 ATACAGGATTTGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hellyer TJ, You Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-620683/67.
                                                                                                                                                                          Local Similarity
les 13, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2003
05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN84687;
                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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                                                                                                                                                                                                                                                                                The invention relates to a polynucleotide comprising an RNA sequence. The bolynucleotides, vector, libraries, and method are useful in lowering the amount of RNA and/or protein production in cells used in drug development process. The present sequence represents a knock-down target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a general primer or primer pair for amplifying and detecting or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes. The general primers are useful for amplifying cervical-neoplasia related HPV genotypes including oncogenic high-risk groups and low-risk groups. The general primers are useful for producing amplifying products to DNA of scores of diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New general primer or primer pair, useful for amplifying and detecting, or for use in a nucleic acid amplification process for amplifying Human Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                          and/or
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                                                                                                                                                                     New knockdown sequences, useful in lowering the amount of RNA protein production in cells used in drug development process.
                                                                    Mesic E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Human Papillomavirus genotype; cervical-neoplasia;
oncogenic high-risk group.
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 5 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
                                                               Clasen RJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        44.8%; Score 13; 100.0%; Pred. No.
                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 259; 402pp; English.
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                                                                 Djokic K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 5; 71pp; English.
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GALAPAGOS GENOMICS NV. VAN DER SCHUEREN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ27975 standard; DNA; 24 BP.
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31-JUL-2003; 2003KR-00053147.
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                                                                 Lambrecht MJY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
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                                                           Arts GJF, Lambrecht MJY Griffioen S, Berge CJL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus
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                                                                                                                            WPI; 2004-775940/76
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ADQ27975;

Query Match

Matches

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genotypes.

Lee S,

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and probes are useful for detecting multiple HIV-1 genotypes, and provide real-time detection of HIV-1. (Updated on 29-AUG-2003 to standardise OS field)
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Sequence 41 BP; 10 A; 11 C; 11 G; 9 T; 0 U; 0 Other;

ö 0; Gaps Query Match

44.8%; Score 13; DB 6; Length 41;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 13; Conservative 0; Mismatches 0; Indels

12 GGTAGATACAGGA 24 |||||||||||| 23 GGTAGATACAGGA 35

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Search completed: March 5, 2006, 22:33:21 Job time: 275.5 secs

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Perfect score:

Run on:

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Searched:

Score

8

0 0 0 0 0 0

Result

Gaps

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Indels

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                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                                                                                65 bp DP Sequence 2375 from Patent WO0210449. CQ532740 GI:41499004
Mismatches
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                             10 GTTACCATAGAGC 22
Conservative
                                                 19 GTTACCATAGAGC 7
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Matches 13; Conserv
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13;
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                                                                                                         RESULT 3
CQ532740/c
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SOURCE
ORGANISM
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AUTHORS
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Submitted (10-NOV-1994) P.M. Appasamy, Pittsburgh Cancer Institute,
University of Pittsburgh, DeSoto and O'Hara Streets, Pittsburgh,
Pennsylvania PA 15213, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang, L.
Expression of diverse and functional TCR V gamma 4 and V gamma 6
transcripts with N region diversity in fetal liver cells cultured
with interleukin 7
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appasamy, P.M., Weng, Y., Kenniston, T.W., Albert, B.D., DeLeo, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:10090"
/cell type="liver cells cultured without interleukin 7"
/tissue_type="liver"
                                                                                                                                                                         Gaps
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diversity region; immunoglobulin; joining region; N region;
variable region.
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0
             /note="complementarity determining region 3"
/codon_start=1
/product="immunoglobulin heavy chain"
/protein id="AAX90362.1"
/db_xref="G1:62634982"
/translation="CARLYGNYAMDYWGQGTSVTVSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.8%; Score 13; DB 9; Length 31; 100.0%; Pred. No. 4.8e+03;
                                                                                                                                      ch 48.1%; Score 14; DB 9; Length 69; 1 Similarity 100.0%; Pred. No. 1.1e+03; 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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/gene="IgH"
/note="V region"
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Mus musculus
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/note="J region"
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"gene="Igh"
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                                                                                                                                                        Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
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Loyarsov
Losses 1 to 69)
Ivanov,I.I., Schelonka,R.L., Zhuang,Y., Gartland,L.L., Zemlin,M.
and Schroeder,H.W. Jr.
Direct Submission
Submitted (13-JAN-2005) Departments of Microbiology, Pediatrics and
Medicine, University of Alabama at Birmingham, 1530 3rd Ave S,
Birmingham, AL 32294-3300, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AISYS/39 69 bp mRNA linear ROD 19-JUN-2005
Mus musculus clone III0428F immunoglobulin heavy chain (Igh) mRNA,
partial cds.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 69)
Ivanov,I.I.; Schelonka,R.L., Zhuang,Y., Gartland,G.L., Zemlin,M.
and Schroeder,H.W. Jr.
Development of the Expressed IG CDR-H3 Repertoire Is Marked by
Procusing of Constraints in Length, Amino Acid Use, and Charge That
Are First Established in Early B Cell Progenitors
J. Immunol. 174 (12), 7773-7780 (2005)
PAT 30-JAN-2004
                                                                                                                                                                                        Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buachontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                               Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome patent: WO 0210449-A 2375 07-FBB-2002;
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   linear
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100.0%; Pred. No. 4.4e+03;
tive 0; Mismatches 0;
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PAT 23-JAN-2004
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                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human brain
Patent: WO 0157275-A 13783 09-AUG-2001;
                                                                                                      probes useful for
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                                                                                                                                                                                                                      /mol_type="unassigned DNA"
/db xref="taxon.9606"
/note="MAP TO AC009225.1
EXPRESSED IN LUNG, SIGNAL = 1.1
NT HIT: 914501912, EVALUE 2.00e-28
EST_HUMAN HIT: AA091091.1, EVALUE 7.90e-01"
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EXPRESSED IN BRAIN, SIGNAL = 0.86
NT HIT: g14501912, EVALUE 2.00e-28
BST_HUMAN HIT: AA091091.1, EVALUE 7.90e-01"
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                                                                             Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid panalysis of gene expression in human lung Patent: WO 0186003-A 13617 15-NOV-2001; Aeomica, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                             44.8%; Score 13; DB 6; L/
100.0%; Pred. No. 4.3e+03;
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100.0%; Pred. No. 4.3e+03;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
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Location/Qualifiers
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                                                     Hominidae; Homo.
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CQ339689/c
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AR574640
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
Parent: WO 0157276-A 14093 09-AUG-2001,
Aeomica, Inc. (US)
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EXPRESSED INDEX AC00912.5.1
NT HIT: 914501912, EVALUE 2.00e-28
EST_HUMAN HIT: AA091091.1, EVALUE 7.90e-01"
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                                                                                                                                                                                                    t="immunoglobulin heavy chain"
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100.0%; Pred. No. 4.4e+03
iive 0; Mismatches C
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Sequence 13617 from Patent WO0186003.
CQ302512.
CQ302512.1 GI:41263089
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Location/Qualifiers
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CQ144071/c
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CQ302512/c
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PAT 15-MAY-2001

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robbins,J.M. and Tritz,R. Ribozyme therapy for the treatment of proliferative skin and eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.4%; Score 12; DB 6; Length 19; 100.0%; Pred. No. 2.1e+04; vative 0; Mismatches 0; Indels
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/noTee="PCNA HH ribozyme binding site"
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Patent: WO 0130362-A 3968 03-MAY-2001;
IMMUSOL, INC. (US)
Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                1. .19
/organism="unknown"
/mol_type="genomic DNA"
Location/Qualifiers
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Best Local Similarity 100.
Matches 12; Conservative
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AX132750
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Unclassified.
1 (bases 1 to 19)
Robbins, J.M. and Tritz, R.
Ribozyme therapy for the treatment of proliferative skin and eye diseases
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Unclassified.
1 (bases 1 to 19)
Robbins,J.M. and Tritz,R.
Ribozyme therapy for the treatment of proliferative skin and eye
diseases
                                                              Unclassified.
1 (bases 1 to 19)
Robbins,J.M. and Tritz,R.
Ribozyme therapy for the treatment of proliferative skin and eye
diseases
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100.0%; Pred. No. 2.1e+04;
tive 0; Mismatches 0; Indels
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41.4%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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Sequence 3969 from patent US 6770633.
AR574641
                                                                                                                                             Patent: US 6770633-A 3968 03-AUG-2004;
Immusol, Inc.; San Diego, CA
Location/Qualifiers
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Immusol, Inc.; San Diego, CA
Location/Qualifiers
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Immusol, Inc.; San Diego, CA
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US 6770633.
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Sequence 3970 from patent
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ARS74642.1 GI:56575534
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   AR574640.1 GI:56575532
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PAT 15-MAY-2001

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Score 12; DB 6; Length 23; Pred. No. 2e+04;

Mismatches

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Search completed: March 6, 2006, 00:38:42
Job time : 1170.5 secs
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100.0%; Pr.
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Best Local Similarity 100.
Matches 12; Conservative
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Inhibition of TACE or amphiregulin for the modulation of EGF
receptor signal transactivation
Patent: EP 1449538-A 9 2.5-AUG-2004,
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                       Robbins, J.M. and {\tt Tritz,R}. Ribozyme therapy for the treatment of proliferative skin and eye diseases
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/note="dT
Description of Artificial Sequence:siRNA"
                                              Length 19
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IMMUSOL, INC. (US)
Location/Qualifiers
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other sequences; artificial sequences.
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Seguence 3970 from Patent W00130362.
AX132752
                                         Query Match 41.4%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 2.1 Matches 12; Conservative 0; Mismatches
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Sequence 9 from Patent EP1449538.
CQ855710
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Ullrich, A., Gschwind, A. and Hart, S.
Inhibition of tace or amphiregulin for the modulation of egf
receptor signal transactivation
Batent: WO 2004073734-A 9 02-SBP-2004;
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
  PAT 13-SEP-2004
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Description of Artificial Sequence:siRNA"
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Sequence 670021,
Sequence 16386, A
Sequence 350520,
Sequence 176713,
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2111, Ap
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Sequence 207943,
Sequence 473578,
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                                                                              5, 2006, 22:21:59 ; Search time 360 Seconds (without alignments) 666.144 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-927-046-382
US-09-927-046-1794
US-10-720-424B-5
US-10-720-424B-5
US-10-681-773-6313
US-10-681-773-60170
US-10-681-773-60170
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US-10-719-900-473578
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APPLICANT: Kim, Seung-Jo
APPLICANT: Kim, Seung-Jo
APPLICANT: Cha, Kwang-Yul
APPLICANT: Cha, Kwang-Yul
APPLICANT: Cha, Kwang-Yul
APPLICANT: Ko, Jung-Jae
TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
FILE REPRENCE: NEITOOUS
CURRENT APPLICATION NUMBER: US/10/720,424B
CURRENT APPLICATION NUMBER: KR10-2002-0075370
PRIOR APPLICATION NUMBER: KR10-2003-0053147
PRIOR FILING DATE: 2002-11-29
PRIOR FILING DATE: 2003-07-31
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Sequence 1, Appli
Sequence 21, Appl
Sequence 383, App
Sequence 1572, Ap
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Sequence 117639,
Sequence 224019,
Sequence 79313, A
Sequence 759047,
Sequence 759047,
Sequence 759047,
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Sequence 35481
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Sequence 57119,
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APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
US-10-719-900-453770
US-10-719-900-919771
US-10-956-157-117639
US-10-956-157-117639
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US-10-294-957-21
US-09-927-046-383
US-09-927-046-1572
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US-10-119-900-207943
Sequence 207943, Application US/10719900
Publication No. US20050026164A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10720424B Publication No. US20040248085A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
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APPLICANT: Lee, Sang-Wha
APPLICANT: Kim, Yeon-Soo
APPLICANT: Yu, Kang-Yeol
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Best Local Similarity
Matches 29; Conserv
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; Sequence 350520, Application US/10719956; Publication No. US20040146910A1; GENERAL INFORMATION:
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                         27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 GATATGGTAGATACA 25
                                                            3 GTAGATACAGGATTT 17
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Matches 14; Conservative
                           13 GTAGATACAGGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Mus musculus
US-11-036-317-670021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-16386
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US-10-719-956-350520/c
                                                                                                                  RESULT 5
US-11-036-317-670021
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LENGTH: 25
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Sequence 493325, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
TITLE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xue Med Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 35.24
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 06/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 473578
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION WUMBER: 60/427,808
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: M.Croarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 207943
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.7%; Score 15; DB 8; Length 25; ilarity 100.0%; Pred. No. 1.3e+02; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                               Length 25;
                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                   .3e+02;
                                                                                                                                                                                                                               DB 8;
                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                 Score 15;
Pred. No.
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; Sequence 473578, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INPORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                         ; ORGANISM: Mus musculus US-10-719-900-207943
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CORGANISM: Mus musculus
US-10-719-900-473578
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US-10-719-900-493325
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Best Local Similarity
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LENGTH: 25
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Sequence 670021, Application US/11036317
Fublication No. US20050214823A1
Fublication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
TITLE REFERENCE: 3654.1
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRIOR APPLICATION NUMBER: US 60/536,639
FRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOSTWARE MIGRARIARY Probe Sequence Listing Generator V 1.1
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US-10-098-263B-16386/C
US-10-098-263B-16386/C
Sequence 16386, Application US/10098263B
Sequence 16386, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT PILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR PILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGIH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 51.7%; Score 15; DB 10; Length 25; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
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APPLICANT: Ayers, Dave
APPLICANT: Grupe, Andrew
APPLICANT: Szymkowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor
TITLE OF INVENTION: Channel-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Szymkowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor:
TITLE OF INVENTION: Channel-1
                                                                                                                                                                               Gaps
                                                    ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043853
US-10-257-017B-176714
                                                                                                                        44.8%; Score 13; DB 8; Length 13; 100.0%; Pred. No. 1.8e+03; ive 0; Mismatches 0; Indels
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; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
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Publication No. US20030064946A1
GENERAL INFORMATION:
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Publication No. US20030064946A1
     ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 76.99
Matches 10; Conservative
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4 AUGGUAGAUACAG 16
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Thompson, Jim
McKenzie, Tim
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Thompson, Jim
McKenzie, Tim
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                                                                                                                                                                                                                                                                     13 GGTGATATGGTAG 1
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; ORGANISM: Homo sapiens
US-09-927-046-382
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                                                                                                                                                 Best Local Similarity
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                                                                                                                           Query Match
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APPLICANT:
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APPLICANT:
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single mucleotide polymorhphisms (SNPs) and cytosine
FILE REPERENCE: BOL/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR PELING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: B01/1133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PILIATION NUMBER: DE 10019173.8
PRIOR FILIATION DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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US-10-257-017B-176713
                                                                                          NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 350520
LENGTH: 25
                                                                                                                                                                                                                                                                                            Length 25;
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1.8e+03;
CURRENT APPLICATION NUMBER: US/10/719,956 CURRENT FILING DATE: 2003-11-20
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8est Local Similarity 100.0%; Pred. No. Matches 13; Conservative 0; Mismatc
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                    CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
                                                                                                                                                                                                                                                                                    Query Match 48.3%; Soc
Best Local Similarity 100.0%; P.
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                , ORGANISM: Rattus norvegicus US-10-719-956-350520
                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GGTGATATGGTAGA 5
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LENGTH: 13
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LENGTH: 13
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US-12-081-7/3-303/C

Sequence 3553, Application US/10681773

Publication No. US20040146890A1

GENERAL INFORMATION:

APPLICANT: Matsuzaki, Hajime

APPLICANT: Matsuzaki, Hajime

APPLICANT: Shen, Mei, Rui

APPLICANT: Shen, Mei, Mei

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans

TITLE OF INVENTION: 152.2.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR PILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 124031

SEQ ID NO 3553

LENGTH: 25
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US-10-681-73-60170/C

j Sequence 60170, Application US/10681773

j Publication No. US20040146890A1

j GENERAL INFORMATION:
    APPLICANT: Meteuzaki, Hajime
    APPLICANT: Meteuzaki, Hajime
    APPLICANT: Mei, Rui
    APPLICANT: Shen, Mei-Mei
    APPLICANT: APPLICANTON NUMBER: US/10/681,773
    CURRENT FILING DATE: 2003-10-07
    PRIOR APPLICATION NUMBER: 60/470,475
    PRIOR APPLICATION NUMBER: 60/470,475
    PRIOR APPLICATION NUMBER: 60/470,475
    PRIOR APPLICATION NUMBER: 60/417,190
    PRIOR APPLICATION NUMBER: 00/417,190
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O. 1.8e+03; Indels
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                                   Indels
      Best Local Similarity 100.0%; Pred. No. 1.8e+03; Matches 13; Conservative 0; Mismatches 0;
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100.0%; Fr.
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Best Local Similarity 100.0%; P. Matches 13; Conservative 0;
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-681-773-3553
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US-10-681-773-60170
                                                                                                                                                                                                                                                         RESULT 14
US-10-681-773-3553/c
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                                                                                                                                                                                                                                                                                                                         Sequence 2111, Application US/09927046

Sequence 2111, Application US/09927046

Publication No. US20030064946A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: McKenzie, Tim

APPLICANT: McKenzie, Tim

APPLICANT: Apers, Dave

APPLICANT: Apers, Dave

APPLICANT: Szymkowski, Edmund

TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori

TITLE OF INVENTION: Channel-1

FILE REFERENCE: 249/021

CURRENT FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 5450

SOFTWARE: PatentIn Version 3.0

SEPTIMES PATENTING DATE: APPLICANTION OF SEQ ID NOS: 5450

SOFTWARE PATENTING DATE: APPLICANTION OF SEQ ID NOS: 5450

SOFTWARE PATENTING DATE: APPLICANTION OF SEQ ID NOS: 5450
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| Sequence 5. Application No. US20040248085A1
| Septence 1. No. US20040248085A1
| GENERAL INFORMATION:
| APPLICANT: ALBIOMED CO., LTD
| APPLICANT: Kim, Yeon-Soo
| APPLICANT: Kim, Seung-Wha
| APPLICANT: Kim, Seung-Yul
| APPLICANT: Kim, Seung-Yul
| APPLICANT: Ko, Jung-Jae
| APPLICANT: Ko, Jung-Jae
| TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
| TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
| TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE OF
| TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE OF
| TITLE OF INVENTION UNMBER: KR10-2002-0075370
| FILE REFERENCE: 2003-11-24
| FRIOR APPLICATION NUMBER: KR10-2003-0053147
| FRIOR APPLICATION NUMBER: RR10-2003-0053147
| FRIOR FILING DATE: 2003-07-31
| NUMBER OF SEQ ID NOS: 16
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 5
| LEMETH: 24
| LEMETH: 24
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   44.8%; Score 13; DB 3; Length 17; 76.9%; Pred. No. 1.8e+03; Live 3; Mismatches 0; Indels
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Pred. No. 1.8e+03;
3; Mismatches 0;
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ORGANISM: Human Papillomavirus
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Best Local Similarity 76.9%;
Matches 10; Conservative
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Query Match
Best Local Similarity 76.9
Matches 10; Conservative
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US-09-927-046-2111
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Gaps

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Search completed: March 5, 2006, 23:01:34 Job time : 361 secs Cal Arbia egod sin:

Perfect score:

Sequence:

Aword size

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AG251154 Lotus cor
AV956811 AV956811
AZ345739 1M008006
CN857089 000722AAA
BH186923 032 P 09-
CG577082 057212495
AL623869 T7 end of
BU653687 1112108C1
CD944463 RDI 67 Ge
CL446082 PST2274-N
BH683741 SALK 0781
BP048125 BP048125
BU822313 UB35DP801
CG620161 OST316914
AW19280 CM2-ST009
AW899633 RC4-NN008
CX054323 tai97h03
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CZ487828 f05203-3p
AI377540 tc15g07.x
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/cell_type="Epithelial"
/cell_line="T470"
/clone_lib="Genetrap T47D Human Breast Carcinoma Library"
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
1 (bases 1 to 74)
Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M.,
Bernardino,A., Durick,K. and Pollok,B.
Exon-trap tags from a T47D GenomeScreen(TM) Library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
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/db_xref="taxon:9606"
AZ665106
CD398050
AG251154
AV956811
AV956811
CG374582
CG577082
CG577082
CG577082
CG577082
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AZ771784
TA19671784
AM179280
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                                                                                                                                                                             Contact: Greg Henkel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Tel: 8584048436
Fax: 8584046719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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VERSION
KEYWORDS
SOURCE
ORGANISM
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COMMENT
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AUTHORS
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CR260472 Forward 6
BZ291460 SALK 1207
BG932614 h81-64 h8
AZ919663 1006016B0
CB27455 mai69c08.
CNS63098 taf83b02.
CC740007 S1LB06a25
CC211033 4012004G0
CC735002 S1LE04c10
BH864657 SALK 0965
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AZ829961 ZM0107122
AZ289007 Q186h06.x
BMZ85347 pb12906.y
AV770608 AV770608
AZ770601 BP916081
CG522729 OST92796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                            5.1.7
Biocceleration Ltd.
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                          GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
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CB274455
CN563098
CO740007
CZ911033
CO735002
BH864657
                                                                                                                           nucleic search, using sw model
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AV770608
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AI289007
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gb_htc:*
gb_est5:*
gb_est6:*
gb_est7:*
gb_est7:*
gb_gss3:*
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gb_est2:*
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Class: TDNA tagged
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Best Local Similarity
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    COMMENT
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/note="Organ: Breast; Vector: pAmp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and used to transform DH5-alpha competent bacteria."
                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                   CR260472 55 bp DNA linear GSS 06-JUL-2004 Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN342d22, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 55)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Direct Submission
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

( Dases I to 66)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeeke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                           Gaps
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hes 0;
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1.8e+03;
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                                                                                                Query Match

48.3%; Score 14; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 14; Conservative 0; Mismatches
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/organism="Mus musculus"
/ol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="WHPN43422"
/clone_lib="WHPN"
                                                                                                                                                                                                                                                                                                                                                                                                                   GSS; genome survey sequence; MICER Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                            CR260472
CR260472.1 GI:50039325
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Best Local Similarity 100.
Matches 13; Conservative
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CR260472/c
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BZ291460
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/db xref="taxon:3702"
/db xref="taxon:3702"
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/clone="lb="hrabidopsis thaliana TDNA insertion lines"
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Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 8579
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG932614
h81-64 h81 S. mansoni adult mini-library,
Fietto/DeMarco/Verjovski-Almeida Schistosoma mansoni cDNA, mRNA
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Use of degenerate primers and touchdown PCR for construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="BH"
/strain="BH"
/db_xref="taxon:6183"
/dev_stage="Adult"
/clone lib="h81 S. mansoni adult mini-library,
Fietro/DeMarco/Verjovski-Almeida"
/note="Vector: Bluescript SK; minilibrary constructed
using low-stringency RT-PCR and consensus-degenerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 83)
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Contact: Verjovski-Almeida, Instituto de Quimica
Departmento de Bioquimica, Instituto de Quimica
Universidade de Sao Paulo
Av. Lineu Prestes, 748, Sao Paulo, SP 05508-900, Brasil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 66;
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                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .83
/organism="Schistosoma mansoni"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biotechniques 32 (6), 1404-1408 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 55-11-3091-2173
Fax: 55-11-3091-2186
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Schistosoma mansoni
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Euteleostomi;

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RESULT 5 AZ919663

ઠે 셤 ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

TITLE JOURNAL COMMENT REFERENCE AUTHORS

FEATURES

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/ Usaue type="appermatocytes, pooled from multiple mice"
/ dev stage="60 day"
/ lab host="bl108 (phage-resistant)"
/ lab host="bl108 (phage-resistant)"
/ clone lib="McCarrey Eddy spermatocytes"
/ note="Organ: testis; Vector: pBluescript SK+
(Stratagene); Site l: XhoI; Site 2: BCoRI; CDNA oligo
dT-primed [5'-(GA)Î0-ACTAGTCTCGAGTTTTTTTTTTT-3'] and
directionally cloned using 5' linkers 5'-AATTCGCAGCAGG,
and 5'-CTCGTGCCG-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambde UniZAP-KR) and resulting
single-stranded phagemids were prepped and tranformed
into DH10B. Library contains 98 recombinants.
References 1, Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E. M. Bddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4413 14 286 1800
Email: est@waison.wustl.edu
Library constructed and donated by J. McCarrey, Ph.D. (Southwest
Foundation for Biomedical Research, Dept. of Genetics) - excision
done by E.M. Eddy, Ph.D. (National Institutes of Health, National
Institute of Environmental Health Sciences).
MGI:2070662
                                                                                                                                                                                                                                                                                  1 (bases 1 to 99)
McCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
Mattin,J., Wylle,T., Dante,M., Bowers,Y., Theising,B., Gibbons,M.
Ritter,E., Tsagareishuli,R., Ronko,I., Maguire,L., Kennedy,S.,
Bennett,J., Waterston,R. and Wilson,R.
mai69c08.y1 McCarrey Eddy spermatocytes Mus musculus cDNA clone IMAGE:6446702 5', mRNA sequence.
                                                                                                                                                                                              Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: McCarrey/Eddy NIEHS Mouse NIEHS Mouse
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:10090"
clone="IMAGE:6446702"
                                                                                                                                            Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="CD-1"
                                                                                   CB274455.1 GI:28464778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
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// dev stage="adult"
// dev stage="adult"
// lab/host="alult]
// lab/host="lult]
// lab/host="lult]
// lab/host="lult]
// lab/host="lult]
// lab/host="lult]
// lab/host="alub/host]
// site l: BamHI; site 2: BglII;
// RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
// Mu elements insert preferentially into transcription
units: For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu. Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BgIII, and ligated to form circular plasmids. DHIOB
cells were transformed and then screened on LB plates with
ampicillin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. (bases 1 to 85)
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1006016B04.x1 1006 - RescueMu Grid G Zea mays genomic, genomic guryey sequence.
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cultivar="mixed background W23/A188/B73"
db_xref="taxon:4577"
                                                           Length 83;
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44.8%; Score.13; DB 9; Length 85;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Pax: 650 723 2227
                                                     DB 2; Len
6.9e+03;
hes 0;
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                                                     44.8%; Score 13; DB 100.0%; Pred. No. 6.9 ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: walbot@stanford.edu
Plate: 1006016 row: 41
Class: transposon-tagged.
Location/Qualifiers
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AZ919663.1 GI:13389597
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Walbot
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CZJILUJJ GSS 08-AUG-2005
4012004G06.2EL yl 4012 - RescueMu Grid BB Zea mays genomic, genomic
survey sequence.
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Microarray analysis of transcriptional changes during hibernation
in the golden mantled ground squirrel, Spermophilus lateralis
Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="brain"
/dev_stage="Adult"
/lab_host="E.coli Blectromax DH10B"
/clone_lib="squirrel brary 1"
/note="Vector: prriplEx2; Site 1: Sfil GGCCATTACGGCC;
Site 2: Sfil GGCCCCTCGGCC; Normalized cDNA library
prepared from brain of hibernating and summer animals"
                                                                       Contract: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4431
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 25 row: 1 column: 03
Seq primer: TriplEx 5'LD (5'-CTCGGGAAGCGCGCATTGTGTTGGT-3')
High quality sequence stop: 41.
Location/Qualifiers
                                                                                                                                                         Crown
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/cultivar="mixed background W23/A188/B73/K55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                      1..41
/organism="Spermophilus lateralis"
/mol_type="mRNA"
/db_xref="taxon:76772"
/clone="25103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.4%; Score 12; DB 7; Le
100.0%; Pred. No. 2.6e+04;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          855 California Ave, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Biological Sciences
Stanford University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male & female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: transposon-tagged.
Location/Qualifiers
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Fax: 650 725 8221
Email: walbot@stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 43) Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
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CZ911033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Konstantin Khalturin, Zoologisches
Institut, Univ. Kiel, Germany Library materials provided by Thomas
Bosch, Zoologisches Institut, CAU Kiel, Germany DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Hans Bode (hrbode@uci.edu)
Putative full langth read
vector to vector length is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Hydra EST -Kiel 1"
/note="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I;
pSPORT 1 Vector is ampicillin resistent, MI3 reverse
primer was used by us for sequencing of 5; parts of
inserts; 3; parts of cDNAs contain long polyA tracks which
makes sequencing from 3' direction complicated"
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                                                                                                                                                                          Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae; Hydridae; Hydra.
Hydridae; Hydra.
L basea I to 100)
Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q., Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M., Hiller, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Tsagareishvili, R., WashU Hydra EST Project
WashU Hydra EST Project
Other ESTS: taf63b02.y2
Contact: Hans Bode
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Spermophilus lateralis
Bukaryotas, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Sciuridae; Xerinae; Marmotini; Spermophilus.
       to SW:RLA2_BRAFL 001725 60S ACIDIC RIBOSOMAL PROTEIN P2. ;, mRNA
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Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
Rogers, J. and Cossins, A.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="105"
/db_xref="taxon:6085"
/lab_host="DH5a"
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Location/Qualifiers
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CO740007
CO740007.1 GI:50827277
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                                                                                 CN563098.1 GI:46972402
                                                                                                                                  Hydra magnipapillata
Hydra magnipapillata
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BH864657 Arabidopsis thaliana TDNA linear GSS 05-AUG-2002 SALK 096549 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_096549, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shina, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="SALK 096549"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the prococols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g79990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
              Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 46;
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100.0%; Pred. No. 2.6e+04;
vative 0; Mismatches 0;
        41.4%; Score 12; DB 7; L
100.0%; Pred. No. 2.6e+04;
live 0; Mismatches 0;
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/mol_type="genomic DNA"
/ecotype="Col-0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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           Query Match
Best Local Similarity 100.
Matches 12; Conservative
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Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,

Rogers, J. and Cossins, A.R.

Microarray analysis of transcriptional changes during hibernation in the golden mantled ground squirrel, Spermophilus lateralis Contact: Andrew R. Cossins

Lonpublished (2004)

Contact: Andrew R. Cossins

Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 7ZB

Tel: +44(0)151-795-4510

Fax: +44(0)151-795-4431

Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 10 row: g column: 02
Seq primer: pflc T7 (5'-AATAGGACTCACTATAGGG-3')

High quality sequence stop; 46.

Location/Qualifiers
/dev_stage="adultar"
/lab_host="adultar"
/lab_host="bild"
/clone_lib="4012 RescueMu Grid BB"
/clone_lib="4012 RescueMu Grid BB"
/clone_lib="4012 RescueMu (engineered from hote="Organ: last; Vector: RescueMu (engineered from hote="color: last; Vector: RescueMu (engineered from pBblueScript backbone); Site 1: BamHI; Site 2: BglI; RescueMu to al.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/. Grid BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B calls were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                    Grid
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Spermophilus lateralis
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Sciuridae; Xerinae; Marmotini; Spermophilus.
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/lab_host="E.coli Blectromax DH10B"
/clone_lib="squirrel embryo library 1"
/note="Vector: pFLC; Site 1: SalI GTCGAG; Site_2: BamHI
GGATCC; Normalized and subtracted cDNA library prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CO735002 46 bp mRNA linear EST 29-JUL-2
SILEO4c10g02f1 squirrel embryo library 1 Spermophilus lateralis
CDNA clone 10g02 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.4%; Score 12; DB 10; Length 43; 100.0%; Pred. No. 2.6e+04; ive 0; Mismatches 0; Indels
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/mol_type="mRNA"
/db_xref="taxon:76772"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male and female"
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CO735002.1 GI:50822272
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Matches 12; Conserv
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CO735002/c
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Gaps

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/note="Vector: sCos-1; Human Chromosome 11 specific cosmid
library prepared from flow sorted human Chromosome 11
derived from Chinese Hampster Ovary (CHO) monochromosomal
somatic cell hybrid, J1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ345736 1000 plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080M03 R, genomic survey sequence.
                                                                                                                     Hominidae, Homo.

1 (bases 1 to 53)
Evans,G.A., Burbee,D., Davies,C., Hahner,L., Oliver,T., Gilbert,M., Jones,D., Ward,T., Gillian,E., Schagemann,J., Probst,S., Harris,J., DeFord,J., McFarland,J., Burzinski,K., Khan,M., Kupfer, K. and Garner,H.R.
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
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                                                                                                                                                                                                                                                                   Genomic Sequence Sampled Map of Chromosome 11
Unpublished (1996)
Contact: Evans GA, Shane Probst
Contact: Evans GA, Shane Probst
University of Texas Southwestern Medical Center At Dallas 5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/db_xref="taxon:9606"
/clone="cSRL-157G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 53.
Location/Qualifiers
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Mus musculus
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                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T7
Class: cosmid ends
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                                                Homo sapiens
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S Striathow, N., Li, Y., Rosso, M.G. and Weisshaar, B.

Direct Submission

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

This sequence has been recovered from the lett border of the T-DNA.

It indicates an insertion within the locus defined by BAC clone

F9D24. Details on the protocols used for generation of the sequence

are described in References 1-3. The sequences are generated at the

MPI for Plant Breeding Research in the context of the GABI-Kat

project. GABI-Kat is part of the German Plant Genomics program

designated 'GABI- Information on line availability can be found

at: http://www.mpiz-koeln.mgg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ecotype="Col-0" f / note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pGABII (GenBank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(6) resulting from the PCR were directly sequenced tearment the genomic sequence flanking the insertion. T-DNA derived sequences were removed.
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                                                                                                                                                                                                                                                                                                                                                                                                            An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db xref="texon:3702"
/clone="GK-722B11-025198"
/clone="GK-722B11-025198"
                                                                                                                                                                           Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (RST) database the identification of T-DNA insertion mutants in Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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B02637.1 GI:1411915
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Matches 12; Conserv
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VERSION
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AUTHORS
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                             /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library" /note="Wetcor: PWD42nv; Purified genomic DNA from M. musculus C57BL/64 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sohn, D.S. Park, C.M.Lee, W.K. Cho, H.J.Ahn, M.Y.Lee, M.Y.Hwang, S.W.Jin
Laboratory of Molecular Biology
Kyungpook National University
Dept. of Genetic Eng., Kyungpook National Univ., Taegu 702-701,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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1 (bases 1 to 61)
Sohn, U., Park, D.S., Lee, C.M., Cho, W.K., Ahn, H.J., Lee, M.Y., Hwang, M.Y. and Jin, S.W.
Human HTCDL1 library cDNAs
Unpublished (1994)
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KTH167 HTCDL1 Homo sapiens CDNA 5'/3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 41.4%; Score 12; DB 9; Length 54; Best Local Similarity 100.0%; Pred. No. 2.6e+04; Matches 12; Conservative 0; Mismatches 0; Indels
                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 54.
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                                                                                                                                                                                                                                                                                               sex="Male
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Uik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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VERSION
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ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                  FEATURES
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/db xref="XII-Blue"
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41.4%; Score 12; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
Fax: 82-053-955-5327
Email: usohn&bh.kyungook.ac.kr
Seq primer: M13 Reverse/SK primer.
Location/Qualifiers
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REPERENCE: 3590.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR PILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PATENTIN VETSION 3.2
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respended, Angela
APPLICANT: Respended, Angela
APPLICANT: Respended, Angela
APPLICANT: Respended, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Warshall, William
APPLICANT: WINDER: Scaringe, Stephen
ITLE REFERENCE: 13499US
CURRENT FILING DATE: 2003-09-10
PRIOR PELICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEG ID NO 662756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.3%; Score 14; DB 12; Length 50; 100.0%; Pred. No. 88;
                                                                                                                                                                                                    DB 12; Length 25;
86;
  NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Prea. ...
                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                       48.3%; Score 14; 100.0%; Pred. No.
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Best Local Similarity 100.0
Matches 14; Conservative
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Matches 14; Conservative
                                                                                                   TYPE: DNA
CORGANISM: Homo sapien
US-11-121-849-276816
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ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-101-244-662756
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US-11-175-859-93016
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                                                 SEQ ID NO 276816
LENGTH: 25
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Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarrays
FILE OF INVENTION: Microarrays
FILE REPERBNCS: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
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; Sequence 1492736, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
   APPLICANT: Dharmacon, Inc.; APPLICANT: Reynolds, Angela
   APPLICANT: Reynolds, Angela
   APPLICANT: Amerhall, William
   APPLICANT: Amerhall, William
   APPLICANT: Scaringe, Stephen
   TITLE OF INVENTION: Functional and Hyperfunctional siRNA
   TITLE OF INVENTION: Functional and Hyperfunctional
   FILE REFERENCE: 13499US
   CURRENT APPLICATION NUMBER: US/11/083,784
   CURRENT FILING DATE: 2005-03-18
   PRIOR APPLICATION NUMBER: 60/502,050
   PRIOR PELICATION NUMBER: 60/426,137
   PRIOR PELICATION NUMBER: 60/426,137
   RINGR FILING DATE: 2003-11-14
   PRIOR PELICATION NUMBER: 60/426,137
   RINGR FILING DATE: 2003-11-14
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Pred. No. 85;
3; Mismatches 0; Indels
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
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Best Local Similarity 78.6%;
Matches 11; Conservative
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GGUAGAUACAGGAU 17
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US-11-083-784-1492736
                                                                                                                                                                                                                               TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1492736
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LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional BIRNA
FILE REFERENCE: 13499US
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APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROPIECTS
LENGTH: 19
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
                                                                                                                                                                                                                              Sequence 1379350, Application US/11101244 Publication No. US20050246794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khvorova, Anastasia
Reynolds, Angela
                                                                                     17 ATACAGGATTIGG 29
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                         17 ATACAGGATTTGG 5
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US-11-101-244-1379350
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US-11-101-244-1492657
Query Match
Best Local Similarity
Matches 13; Conserv
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                      Length 19;
                                                                 0; Indels
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APPLICANT: Dharmacon, Inc.

APPLICANT: Khvorova, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional sirnA

CURRENT APPLICATION NUMBER: US/11/101, 244

CURRENT PILING DATE: 2005-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                      Score 13; DB 10;
Pred. No. 3.3e+02;
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CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1366068
LENGTH: 19
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Pred. No.
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                                                                                                                                                                                                          RESULT 7
US-11-101-244-662769
Sequence 662769, Application US/11101244
Publication No. US20050246794A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
SUPHRER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
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Best Local Similarity 76.9%;
Matches 10; Conservative
                    Query Match
Best Local Similarity 76.9%;
Matches 10; Conservative
                                                                                                                                    4 AUGGUAGAUACAG 16
                                                                                                       10 ATGGTAGATACAG 22
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5 AUGGUAGAUACAG 17
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US-11-101-244-662769
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US-11-101-244-1366068
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LENGTH: 19
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Gaps

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APPLICANT: KINCOVA, AnaBtasia
APPLICANT: Kaynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLS OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
                                             Score 13; DB 11; Length 19;
Pred. No. 3.3e+02;
3; Mismatches 0; Indels
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Sequence 1366068, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION,

APPLICANT: Carranacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Leake, Devin

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US
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3.3e+02;
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CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
FRIOR FILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-09-10
SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
LENGTH: 19
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US-11-083-784-1379350
; Sequence 1379350, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; P.
Matches 13; Conservative 0;
                                                  44.8%;
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5 AUGGUAGAUACAG 17
                                                                                                                                                10 ATGGTAGATACAG 22
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                                             Query Match
Best Local Similarity 76.9
Matches 10; Conservative
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US-11-083-784-1366068
US-11-083-784-662769
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; Sequence 662756, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
   APPLICANT: Deamacon, Inc.; APPLICANT: Reynolds, Angela
   APPLICANT: Reynolds, Angela
   APPLICANT: Applicant Reynolds, Angela
   APPLICANT: Acatings, Stephen
   TITLE OF INVENTION: Functional and Hyperfunctional siRNA
   FILE REFERENCE: 13499US
   CURRENT APPLICATION NUMBER: US/11/083,784
   CURRENT FILING DATE: 2005-03-18
   PRIOR APPLICATION NUMBER: 60/502,050
   PRIOR PELICATION NUMBER: 60/502,050
   PRIOR PELICATION NUMBER: 60/426,137
   PRIOR PELICATION NUMBER: 60/426,137
   RIOR PELICATION NUMBER: 60/426,137
   SOFTHARE: PECPRICATER
   SOFURMER: 1991911
   SOFURMER: 1991911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13; DB 11; Length 19; Pred. No. 3.3e+02;
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  76.9%; Pred. No. 3.3e+02; rative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 62769, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER: OF SEQ ID NOS: 1591911
SEQ ID NO 662769
LENGTH: 19
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1 GUAGAUACAGGAU 13
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Best Local Similarity 76.9
Matches 10; Conservative
  Best Local Similarity 76.9
Matches 10; Conservative
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US-11-083-784-662756
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APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TILL OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499018
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PRILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10-10
PRIOR PILING DATE: 2003-10-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1492657
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-1492657
                                                                                                     Score 13; DB 11; Length 19;
Pred. No. 3.3e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 44.8%; Score 13; DB 11; Length 19; Best Local Similarity 76.9%; Pred. No. 3.3e+02; Matches 10; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         Sequence 1492657, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: CANOROVA, Inc.
APPLICANT: Kivorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                     44.8%;
                                                                                                                                                                                    14 TAGATACAGGATT 26
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                                                                                                   Query Match
Best Local Similarity 69.2*
Matches 9; Conservative
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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1379350
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Search completed: March 5, 2006, 22:48:29 Job time : 450.5 secs Sequence 32639, Sequence 32640, Sequence 32641,

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120976 120978 120977

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Sequence

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Run on:

Sequence:

Searched:

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Sequence 53, Application US/08316293

Patent No. 5484699

GENERAL INFORMATION:
APPLICANT: ABBOTT LABORATORIES
APPLICANT: Thomas G. Laffler
APPLICANT: Ronald L. Marshall
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES USEFUL AS
TITLE OF INVENTION: POR THE AMPLIFICATION AND DETECTION OF HUMAN
TITLE OF INVENTION: POR THE AMPLIFICATION AND DETECTION OF HUMAN
TITLE OF INVENTION: PAPILLOMA VIRUS, AND REALTED KITS AND METHODS.
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
US-09-198-452A-2044

US-09-128-204B-30

US-08-82B-952-2

US-09-396-196G-32627

US-09-396-196G-32638

US-09-396-196G-32640

US-09-396-196G-32641

US-09-396-196G-32641

US-09-396-196G-32641

US-09-396-196G-3129

US-09-396-196G-120975

US-09-396-196G-120975

US-09-396-196G-120977

US-09-396-196G-120977

US-09-396-196G-120977

US-09-396-196G-120977

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US-09-396-196G-120977
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US-07-931-473B-331
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/965,665
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/POCKET NUMBER: 4853.US.P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (708) 937-4884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (708) 937-9556
INFORMATION FOR SEQ ID NO: E
SEQUENCE CHARACTERISTICS:
      CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                       5, 2006, 19:08:04; Search time 78 Seconds (without alignments) 660.888 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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                    GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/ina/1_COMB.seq:*
/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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US-09-396-196G-73518
US-09-396-196G-73519
US-09-396-196G-81905
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-09-513-999C-22225
-09-021-701-1077
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                                                                                                                                                                                                                                                               gatggtgatatggtagatacaggatttgg 29
                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-316-293-53
                                                                                                                                                                                                                                                                                                                                                               1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                     nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                  Scoring-table: Oligo Nuc.
                                                                                                                                                                                                                 US-10-720-424B-1
29
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 100
                                                                                                                                           March
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                                                                                                                                                                                                                                            Perfect score:
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Result ģ MOLECULE TYPE: Other nucleic acid (synthetic DNA)

TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear

Sequence 1 Sequence 1 Sequence 1

JS-09-363-970-11

Sequence Sequence

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RESULT 5
US-09-090-947-13/c
IS-09-090-947-13/c
Sequence 13, Application US/09090947
Sequence 13, Application US/09090947
FACENT No. 6008338
GENERAL INFORMATION:
TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA TITLE OF INVENTION: ENCODING SAME, AND ANTIBODIES THERETO NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
APPLICANT: FONG, Henry K.W.

TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA

TITLE OF INVENTION: ENCODING SAME, AND ANTIBODIES THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.4%; Score 12; DB 2; Length 21; 100.0%; Pred. No. 2.2e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/358,171
FILING DATE: 16-DEC-1994
CLASSIFICATION: 530
ATTONENY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: FONG=2
TELEPRANTION INFORMATION:
TELEPRANT: 202-628-5197
TELEPRAN: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,947
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/358,171
                                                                NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                     ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-7.
TELEFAX: 246633
; INFORMATION FOR SEQ ID NO: 13
; SEQUENCE CHARACTERISTICS:
    LENGTH: 21 base pairs
    "vpg: nucleic acid
    "vpg: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TAGATACAGGAT 25
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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US-09-198-452A-1549

US-09-198-452A-1549

Sequence 3549, Application US/09198452A

Patent No. 655294

GENERAL INFORMATION:

APPLICANF: GETIffals, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering the Preference 19710-003-999

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: 1999-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 3549
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                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harris, Tobin J.
APPLICANT: You, Oimin
APPLICANT: Harris, James M.
TITLE OF INVENTION: Sequences and Methods for Detection of HIV-1
FILE OF INVENTION: Sequences and Methods for Detection of HIV-1
CURRENT APPLICATION NUMBER: US/09/757,207
CURRENT APPLICATION NUMBER: US/09/757,207
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.1
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                                        48.3%; Score 14; DB 2; Length 38; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.8%; Score 13; DB 3; Length 41;
100.0%; Pred. No. 6.4e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-358-171-13/C
; Sequence 13, Application US/08358171
; Retent No. 5763578
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09757207
Patent No. 6770752
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3549
                                                                                                                                                               1 GATGGTGATATGGT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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Matches 13; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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                                             Query Match
Best Local Similarity
Matches 14; Conserv
US-08-316-293-53
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LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Gaps

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41.4%; Score 12; DB 3; Length 25; 100.0%; Pred. No. 2.2e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                Length 25;
                                                                                                                                                                                                                                     2.2e+03;
                                                                                                                                                                                                                Score 12; DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: David Lockhart
APPLICANT: Affwretrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymerix, Inc.
IITLE OF INVENTION: Methods of Genetic Analysis
PILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/396,196G CURRENT FILING DATE: 1999-09-15 PRIOR APPLICATION NUMBER: 60/100,678 PRIOR FILING DATE: 1998-09-17 WUMBER OF SEQ ID NOS: 127806 SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/396,196G CURRENT FILING DATE: 1999-09-15 PRIOR APPLICATION NUMBER: 60/100,678 PRIOR FILING DATE: 1998-09-17 NUMBER OF SEQ ID NOS: 127806 SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73518
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 73519, Application US/09396196G
Batent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: A
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                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; P:
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
                                                                                                                                                                                                                                                                                                         6 TGATATGGTAGA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: mus musculus
                                                                                                                    ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-73518
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US-09-396-196G-81905
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Best Local Similarity
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US-09-396-196G-73519/c
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US-09-396-196G-81905/c
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LENGTH: 25.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36348, Application US/09396196G; Patent No. 6821724; Patent No. 6821724; GENERAL INFORMATION: APPLICANT: Michael Mittmann; APPLICANT: David Mack; APPLICANT: David Lockhart; AFFMICANT: David Lockhart; AFFMICANT: AFFWERTIX, Inc.; TITLE OF INVENTION: Methods of Genetic Analysis; FILE REFRENCE: 3101.1; CURRENT APPLICATION NUMBER: US/09/396,196G; CURRENT FILING DATE: 1999-09-15; PRIOR PELICATION NUMBER: 60/100,678; PRIOR FILING DATE: 1998-09-17; NUMBER OF SEQ ID NOS: 127806; SOFTWARE: FRASESEQ for Windows Version 4.0; SEQ ID NO 36348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12; DB 3; L; Pred. No. 2.2e+03;
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'Sequence 73518, Application US/09396196G
'Patent No. 6821724
'GENERAL INFORMATION:
'APPLICANT: Michael Mittmann
'APPLICANT: David Mack
'APPLICANT: David Lockhart
'APPLICANT: AFFYmetrix, Inc.
'TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 41.4%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 2.5 Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
                                                                 REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: FONG=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
                                                                                                                                                                                  TELEX: 248633
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
                     TTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 12; Conservative
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; ORGANISM: Mus musculus
US-09-396-196G-36348
                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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  FILING DATE:
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Sequence 22225, Application US/09513999C

Sequence 22225, Application US/09513999C

Sexuence 22225, Application US/09513999C

Sexuence 22225, Application US/09513999C

Sexuence 22225, Application US/09513999C

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

PRICANT: Dunas Milne Edwards, J.Y.

PRICANT: Dunas Milne Edwards, J.Y.

PRICANTON NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOOTWARRE: PRICANTED NOS: 36681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.4%; Score 12; DB 3; Length 25; 100.0%; Pred. No. 2.2e+03; ative 0; Mismatches 0; Indels
US-09-396-1966-94665/C

US-09-306-1966-94665/C

Sequence 94665. Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1

CURRENT FALLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 94665
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US-09-021-701-1077/c
; Sequence 1077, Application US/09021701
; Patent No. 6251588
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.4
Best Local Similarity 100.
Matches 12; Conservative
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US-09-513-999C-22225
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US-09-513-999C-2225
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LENGTH: 98
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       41.4%; Score 12; DB 3; Length 25; 100.0%; Pred. No. 2.2e+03; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                               US-09-396-196G-94653/C
; Sequence 94653, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Mack
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR PILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 127806
; SEQ ID NO 94653
LENTH: 25
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US-09-396-196G-94664/C
; Sequence 94664 Application US/09396196G
; Pactent No. 6821724
; GENERAL INFORMATION:
APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFRENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FESTSEQ for Mindows Version 4.0
    Query Match
Best Local Similarity 100.
Matches 12; Conservative
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Matches 12; Conservative
                                                                                                     13 GTAGATACAGGA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: mus musculus
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LENGTH: 25
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                                                           NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods for evaluating oligonucleotide
TITLE OF INVENTION: probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
Kincaid, Robert H.
FRNTION: Methods for evaluating oligonucleotide
FRNTION: probe sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Shannon, Karen W.
APPLICANT: Wolber, Paul K.
APPLICANT: Delenstarr, Glenda C.
APPLICANT: Webb, Peter C.
APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: DEP PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.9%; Scor.
100.0%; Pred. No.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1078, Application US/09021701
Patent No. 6251588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 1097
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEPHONE: 650-852-8063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1077:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.9
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 TAGATACAGGA 24
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COUNTRY: US.
ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-021-701-1077
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.7e+03;
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  US/09/021,701
                                                                                           REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 1097;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INPORMATION FOR SEQ ID NO: 1078:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                        ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,6
                    10-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 TAGATACAGGA 24
APPLICATION NUMBER:
                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
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HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-1078
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                    FILING DATE: 1 CLASSIFICATION:
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US-09-696-791-3968
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2 6/ptodata/1/ina/1_COMB.seq:*
/cgn2 6/ptodata/1/ina/5_COMB.seq:*
/cgn2 6/ptodata/1/ina/6_COMB.seq:*
/cgn2 6/ptodata/1/ina/6_COMB.seq:*
/cgn2 6/ptodata/1/ina/H_COMB.seq:*
/cgn2 6/ptodata/1/ina/H_COMB.seq:*
/cgn2 6/ptodata/1/ina/Pp_COMB.seq:*
/cgn2 6/ptodata/1/ina/Pp_COMB.seq:*
/cgn2 6/ptodata/1/ina/Pp_COMB.seq:*
/cgn2 6/ptodata/1/ina/Pp_COMB.seq:*
/cgn2 6/ptodata/1/ina/Rb_COMB.seq:*
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S-09-396-196G-59285
S-09-396-196G-79525
S-08-190-199A-33
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US-09-422-978-4722
US-07-922-773-4-6
US-07-922-723A-6
US-08-074-275-6
US-08-08-074-275-6
US-08-480-366-6
US-09-22-77A-6
US-09-23-040-8
US-09-413-304-8
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                                                                                                                                                                                                                                                                                                                            1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                         - nucleic search, using sw model
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-Gapop_60.0 , Gapext 60.0
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29
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Match Length
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Maximum DB seq length: 100
                                                                                                               March
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Sequence 46, Appl
Sequence 780, App
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Sequence 1123, Ap
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GENERAL INFORMATION:
APPLICANT: RObbins, Joan M.
APPLICANT: Tritz, Richard
TITLE OF INVENTION: SKIN AND EYE DISEASES
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT PILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3969
LENGTH: 19
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Sequence 3968, Application US/09696791

Patent No. 6770633

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: SKIN AND EYE DISEASES
TITLE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT PILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3968
                                                                                                                                                                                                Sequence 118492
Sequence 46, Api
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Sequence
Sequence
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US-09-396-196G-84796
US-09-336-196G-84813
US-09-396-196G-84813
US-09-396-196G-87420
US-09-396-196G-87421
US-09-396-196G-87421
US-09-396-196G-87421
US-09-396-196G-87421
US-09-396-196G-118491
US-09-396-196G-118491
US-09-396-196G-118491
US-09-45Z-638-46
US-09-45Z-638-46
US-09-45Z-638-46
US-09-43G-196G-118491
US-09-43G-196G-1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
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Best Local Similarity
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US-09-396-196G-79525/C
Sequence 79525, Application US/09396196G
Fatent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: 05/09/396,196G
CURRENT FILING DATE: 1999-09-15
FRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FBateSEQ for Windows Version 4.0
SEQ ID NO 79525
LANGTH: 25
                                                                                                                                              Sequence 59285, Application US/09396196G
Fatent No. 6821724
GENERAL INFORMATION
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: AFFLICANT: AFFLICANT: AFFLICANT: AFFLICANT: AFFLICANT: AFFLICANT: AFFLICANT: AFFLICANT: AFFLICANT: Michael Michael CURRENT AFFLICATION WHERE: US/09/396,196G
CURRENT AFFLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
FRIOR APPLICATION NUMBER: 60/100,678
FRIOR AFFLICATION NUMBER: 60/100,678
FRIOR PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRASESEQ for Windows Version 4.0
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US-08-100-199A-33
'Sequence 33, Application US/08190199A
; Patent No. 5830663
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100.0%; Pre
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Best Local Similarity 100.0%; Pr
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Best Local Similarity 100.
Matches 12; Conservative
                           13 ACCATAGAGCCA 24
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US-09-396-196G-59285
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US-09-396-196G-59285/C
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LENGTH: 25
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Sequence 3970, Application US/09696791

Patent No. 6770633

GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard
ITILE OF INVENTION: SKIN ZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
ITILE OF INVENTION: SKIN ZAMD BYE DISEASES
ITILE OF INVENTION: SKIN ZAMD BYE DISEASES
ITILE OF INVENTION: SKIN ZAMD BYE DISEASES
ITILE REFERENCE: 480124, 407

CURRENT APPLICATION NUMBER: 2000-10-25
NUMBER OF SEQ ID NOS: 4523

SOFTWARE: Patent IN Ver. 2.0

SEQ ID NO 3970

LENGTH: 19
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41.4%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
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                                                                                                                                   Length 19;
                                                                                                                                Query Match 41.4%; Score 12; DB 3; Length 19; Best Local Similarity 100.0%; Pred. No. 9.8e+02; Matches 12; Conservative 0; Mismatches 0; Indels
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Patent No. 682724,
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION WHERE: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION UNBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 22482
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: PCNA HH ribozyme binding site US-09-696-791-3970
                                                                ; OTHER INFORMATION: PCNA HH ribozyme binding site US-09-696-791-3969
                                                                                                                                                                                                                                                 7 GTTACCATAGAG 18
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 12; Conserva
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US-09-396-196G-22482
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Gaps
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Pred. No. 3.8e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Drs. Mihael H. Polymeropoulos
APPLICANT: and Carl R. Merril
APPLICANT: FIVE HIGHLY INFORMATIVE
TITLE OF INVENTION: FIVE HIGHLY INFORMATIVE
TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe, Price, Leblanc & Becker
STREET: Suite 300, 99 Canal Center Plaza
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/922,723A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drs. Carl R. Merril and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Drs. Carl R. Merril an
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/07922723A Patent No. 5369004
                                                                                                                                                                                         Query Match 37.9%; Sc
Best Local Similarity 100.0%; P
Matches 11; Conservative 0;
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REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION: 703 684 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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ATTORNEY/AGENT INFORMATION:
NAME: D.J. Mills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 20
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TYPE: DNA
ORGANISM: Homo Sapiens
                                          FEATURE:
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Sequence 4722, Application US/09422978

Patent No. 6537751

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Cohen, Daniel
APPLICANT: Chunakov, 11ya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US 09/0422, 978
CURRENT FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-11-23
EARLIER PRILICATION NUMBER: US 60/109,732.
EARLIER PRILICATION NUMBER: US 60/082,614
                                                                   APPLICANT: JONES, Peter T.
APPLICANT: WINTER, Gregory P.
TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         PILLSBURY MADISON & SUTRO, L.L.P.
1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 37.9%; Score 11; DB 1. Similarity 100.0%; Pred. No. 3.6 11; Conservative 0; Mismatches
                                                                                                                                                                                                                            STREEF: 1100 New YOLK AVENUE, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,199A
FILING DATE: 13-UUL-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/GB92/01483
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9212419.7
FILING DATE: 11-UNV-1992
RROR APPLICATION DATA:
APPLICATION NUMBER: GB 9117352.6
                      MBLETON, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1998-04-21.
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 4722
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-AUG-1991
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE: NO
US-08-190-199A-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08480366
Patent No. 5721100
GENERAL INFORMATION:
APPLICANT: Drs. Carl R. Werril and
APPLICANT: Mihael H. Polymeropoulos
TITLE OF INVENTION: POLYMORPHIC DNA MARKERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lowe, Price, LeBlanc & Becker STREET: Suite 300, 99 Canal Center Plaza CITY: Alexandria STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DOS TEXT FILE
SOFTWARE: DOS TEXT FILE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,366
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ATTORNEY/AGENT INFORMATION:
NAME: J.G. Mullins
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 71701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: J.G. Mullins
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 7170
TELECOWUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-074-275-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11, Conservative
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STRANDEDNESS: sing
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US-08-480-366-6/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence (Application US/08074275); Patent No. 5468610; Patent No. 5468610; GENERAL INFORMATION: APPLICANT: Dre. Carl R. Merril and APPLICANT: Dre. Carl R. Merril and APPLICANT: THRE HIGHLY INFORMATIVE REPEAT TITLE OF INVENTION: POLYMORPHIC DNA MARKERS NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSE: Lowe, Price, Leblanc & Becker STREET: Suite 300, 99 Canal Center Plaza CITY: Alexandria STATE: Virginia
APPLICANT: Mihael H. Polymeropoulos
TITLE OF INVENTION: TWENTY SEVEN HIGHLY INFORMATIVE
TITLE OF INVENTION: MICROSATELLITE REPEAT
TITLE OF INVENTION: POLYMORPHIC DNA MARKERS
NUMBER OF INVENTION: 63
CORRESPONDENCE ADDRESS: 63
CORRESPONDENCE ADDRESS:
ADDRESSE: Lowe, Price, LeBlanc & Becker
STREET: Suite 300, 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: DOS Text File

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/799,828C

FILING BATE: 19911127

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: D.J. Mills

REGISTRATION NUMBER: 34,506

REFERENCE/DOCKET NUMBER: 717081A

TELECOMUNICATION INFORMATION:

TELECOMUNICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 12314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,275
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/707,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Gaps

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Indels

Length 20;

DB 3; Le . 3.8e+03;

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; OTHER INFORMATION: Description of Artificial Sequence:/No. 6207387e US-09-413-304-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LOUIS J. Elsas II
APPLICANT: LOUIS J. Elsas II
APPLICANT: LOUIS J. Elsas II
APPLICANT: K. Muralidharan
TITLE OF INVENTION: MOLECULAR DIAGNOSTICS FOR GALACTOSEMIA
FILE REFERENCE: 055010.0079
CURRENT APPLICATION NUMBER: US/09/413,304
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.9%; Score 11; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 3.8e+03; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                      Score 11;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-413-304-9/c
'Sequence 9, Application US/09413304
'Patent No. 6207387
'GENERAL INFORMATION:
                                                                                                                                                                                                               11; Conservative
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                  AUTHORS: Polymeropoules
JOURNAL: Nucleic Acids
PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 TAGAGCCACTA
                                                                                                                                                                    Query Match
Best Local Similarity
                                                                              ISSUE: 1991
PAGES: 4018
                                                                                                                           US-09-283-040-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Betent No. 6162604
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR DETERMINING GENETIC
TITLE OF INVENTION: AUTO-INFORMINE DISEASES BY GENOTYPING IL-10, BCL-2, FAS-L, AN
TITLE OF INVENTION: OTHER APOPTOTIC GENES.
FILE REPRENEURS: MSCI.010A
CURRENT APPLICATION NUMBER: US/09/283,040
CURRENT FILING DATE: 1999-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
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                                                                                                                  GENERAL INFORMATION:
APPLICANT: Drs. Mihael H. Polymeropoulos
APPLICANT: and Carl R. Merril
TITLE OF INVENTION: ELEVEN HIGHLY INFORMATIVE
TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        STREET: Suite 300, 99 Canal Center Plaza CITY: Alexandria STATE: Virginia COUNTRY: USA ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/952,277A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34506
REFERENCE/DOCKET NUMBER: 717081C
TELECOMMUNICATION INFORMATION:
TELEBHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.9%; Scc.
100.0%; Pre
                                                                        Sequence 6, Application US/07952277A
Patent No. 5861504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.9
Best Local Similarity 100.
Matches 11; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-283-040-8/c
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LENGTH: 20
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Gaps

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Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring\_table:

Word-size:

Searched:

Database :

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Submitted (131-M2.2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5944170. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated
                                                                                   AA234629 ZT75505.T
CW220438 GCC700 TI
CR217452 Reverse 8
BZ382023 SALK 1177
CW083054 104 425 1
CF660841 CCLM09a32
AZ807027 ZW00069A03
AJ654040 AJ654040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                         AL751479 Arabidops
CG532847 OST117308
BX572204 Arabidops
BX536465 Arabidops
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Arabidopsis thaliana T-DNA flanking sequence GK-445F03-023515,
                         W08501 mb47d12.rl
A1040719 ox26b10.s
CK895114 SGP154364
CK896099 SGP158635
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CK814651 Rasgsc531
AZ609630 1M0434E04
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BX553131 BX553131
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B:
Direct Submission
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Bioinformatics 19 (11), 1441-1442 (2003)
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AL942821 Arabidops
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Biocceleration Ltd.
                                                                                                                                                                                                                                                                           41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 gcgtcagaggttaccatagagccactagg 29
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Copyright (c) 1993 - 2006
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                                                                        nucleic search, using sw model
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                                                                                                                                                                                          /note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC16 I (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed.
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1M0201C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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1 (basea 1 to 78)
1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Railly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Under Will inserts
Unpublished (2000)
                                                                                                                                                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
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/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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Information on line availability can be found at:
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                                                                                                                                                                                                                                                                                                                                                                      44.8%; Score 13; DB 10; L 100.0%; Pred. No. 4.8e+03; ive 0; Mismatches 0;
                                                                        /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/dD_xref="taxon:3702"
/clone="GK-445F03-023515"
                  http://www.mpiz-koeln.mpg.de/GABI-Kat/.-
Location/Qualifiers
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0201C08"
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Location/Qualifiers
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Fax: 801 585 7177
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84112, USA
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                                      FEATURES
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Laboratory Mouse DNR Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gilq73214 gbl/R129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Arabidopsis thaliana T-DNA flanking sequence GK-733D10-025420,
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
from the Jackson
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Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.8%; Score 13; DB 9; Length 78;
100.0%; Pred. No. 4.8e+03;
ative 0; Mismatches 0; Indels
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musculus C57BL/6J (male) was obtained
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Arabidopsis thaliana
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Euteleostomi;

FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The shared adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                           AZ801332 44 bp DNA linear GSS 16-FEB-2001
2M0059E17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0059E17 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 44)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@gonetics.utah.edu
Basrt Length: 10000 Std Error: 0.00
Plate: 0059 row: E column: 17
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Seq primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db xref="taxon:10090"
clone="UUGC2M0059B17"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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72 GAGGTTACCATAG 84
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AZ801332/c
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                                                                                                                                                                    /mol_type="genomic pDR"
/db xref="taxon:3702"
/clone="GK-733D10-025420"
/clone="GK-733D10-025420"
/clone="GK-733D10-025420"
/clone="GK-733D10-025420"
/clone="CR-733D10-025420"
/clone="CR-73D10-025420"
/clone="CR-73D10-025420"
/clone="PCR-was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pGABI1 (GenBank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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CDC1e4 Cri du chat, exon trapped products Homo sapiens genomic clone CDC1e4, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Homlinidae, Homo.

1 (bases 1 to 96)
Church, D.M., Yang, J., Shiang, R., Wasmuth and J.J.
A High Resolution Physical and Transcription map for the Cri du Unpublished (1997)
GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mgg.de/GABI-Kat/. Location/Qualifiers
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2400 Med. Sci. I, UCI-COM, Irvine, CA 92697-1700, USA
Tel: (714)824-6792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.8%; Score 13; DB 11; Length 91; 100.0%; Pred. No. 4.8e+03;
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Email: rshiang@chrom5.hsis.uci.edu
Insert Length: 96 Std Error: 0.00
Class: exon-trapped.
Location/Qualifiers
1. 96
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ool type="genomic DNA"
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/db_xref="taxon:9606"
/clone="CDC1e4"
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Shiang lab
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Homo sapiens
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Submitted (13-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (13-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Suechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone MRC8. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
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                                                                                                                                                                                                             AL768653 1-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-076E01-011920,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Weisshaar,B.
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Weisshaar,B.
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/db_xref="taxon:3702"
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                                       64 CCATAGAGCCAC
   14 CCATAGAGCCAC
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Rosso, M.G., Striatov, N., Li, Y. and Weisshaar, B.

Birect Submission

L Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Suchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At1948700.

Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated 'GABI-Kat information on line availability can be found at:

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                BX288836 69 bp DNA linear GSS 02-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-420D05-018101,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 0;
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12874060
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/db_xref="taxon:3702"
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BX288836
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ACCATAGAGCCA
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INRA Rennes
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Dana Farber Cancer Institute
1 Jimmy Fund May Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5139
Email: Marc Vidal@dfci.harvard.edu
For. the purpose of protein interaction mapping, we generated a C. elegans a normalized library of ORF fused to the AD-encoding sequence of the yeast transcription factor GAL4. Those ORFs derive from the PCR amplification between the predicted (WS9) initiation and termination codons, using the CDNA library AD-wrmCDNA as template This Interacting Sequence Tag IST_WIS_41889 (FO9F7.5)
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/db_xref="taxon:6239"
/db_xref="taxon:6239"
/db_xref="maphrodite"
/de_srage="embryos, Li, L2, L3, L4, adult, dauer"
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/clone_lib="xb-offeemel.0 library"
/note="vector: pDestPC86/Cyh; For the purpose of protein
interaction mapping, predicted protein-encoding ORFs, were
amplified by PCR precisely between the predicted (WS9
version of WormPep) initiation and termination codons,
using a cDNA library (AD-wrmcDNA library - Walhout etal.
Methods Enzymol. 2000;328:575-92) as template. The
resulting 11,984 Gateway cloned ORFs along with the
attempted ones were transfered into a two-hybrid
Destination vector downstream of the vector sequence
encoding the activation domain (AD) of the yeast GAL4
transcription factor. Those constructs were pooled
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Li,S., Armstrong,C.M., Bertin,N., Ge,H., Milstein,S., Boxem,M., Vidalain,P.O., Han,J.D., Chesneau,A., Hao,T., Goldberg,D.S., Li,N., Martinez,M., Rual,J.F., Lamesch,P., Xu,L., Tewari,M., Mong,S.L., Zhang,L.V., Berriz,G.F., Jacotot,L., Vaglio,P., Reboul,J., Hirozane-Kighikawa,T., Li,Q., Gabel,H.W., Elewa,A., Baumgartner,B., Rose,D.J., Yu,H., Bosak,S., Sequerrar,R., Fraser,A., Mango,S.E., Saxton,W.M., Strome,S., Van Den Heuvel,S., Plano,F., Mango,S.E., Gundenhaute,J., Sardet,C., Gerstein,M., Doucette-Stamm,L., Gunsalus,K.C., Harper,J.W., Cusick,M.E., Roth,F.P., Hill,D.E. and
                                                                                                                                                               CK589249

1ST WIS_41889 AD-ORFeomel.0 library Caenorhabditis elegans cDNA 5' similar to P09F7.5, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.

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/organism="Caenorhabditis elegans"

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Insert Length: 75 Std Error: 74.00
Plate: 547 row: 08 column: H
Seq primer: CGCGTTTGGAATCACTACAGG
High quality sequence stop: 74
POLYA=No.
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/strain="N2"
                                                                                                                                                                                                                                               CK589249 GI:40973178
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Contact: Vidal M
                       CCATAGAGCCAC 44
CCATAGAGCCAC
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AUTHORS
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CK589249
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/db_xrefe="taxon:40922"
/clone="Rpi31IT7B"
/tissue_type="whole insect"
/dev_stage="third instar nymph (L3)"
/lab_host="rop10"
/lab_host="rop10"
/clone_lib="Rpi3i"
/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB; aphids incculated on one-week old wheat germinations in test tube under non sterile conditions. experimental condition: short photoperiod (10-hr light/14-hr dark at 120C during 12 days)"
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RpL3i-II-B7 RpL3i Rhopalosiphum padi cDNA clone RpL3iII7B 5', mRNA
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library. Reference - Reboul J, Vaglio P etal C. elegans ORFcome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression. Nat Genet. 2003 May;34(1):35-41. PMID: 12679813)"
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Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidioddea; Aphididae; Aphidini; Rhopalosiphum.

1 (bases 1 to 76)
Tagu.C., Prunier-Leterme,N., Legeai,F., Gauthier,J.P., Duclert,A., Sabater-Munoz,B., Bonhomme,J. and Simon,J.C.
Annotated expressed sequence tags for studies of the regulation of Insect. Biochem. Mol. Biol. 34 (8), 809-822 (2004)
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                     Length 75;
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhopalosiphum padi (bird cherry-oat aphid)
                                                                                                                                                                                                                  41.4%; Score 12; DB 7; Le
100.0%; Pred. No. 1.9e+04;
ative 0; Mismatches 0;
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/strain="h3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF800008.1 GI:37804578
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DEFINITION

ACCESSION

ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

ORIGIN

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/dev stage="adult"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="DH10B"
/clone_lib="1006 - RescueMu Grid G"
/note="Organ: leaf, Vector: RescueMu (engineered from pBlueScript backbone); Site_l: BamHl; Site_2: BgllI;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units: For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHl
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL947277 80 bp DNA linear GSS 02-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-303All-015563,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Borso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At3919680.

Details on the protocols used for generation of the sequence are
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Arabidopsis thaliana
Bubaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                         Length 80,
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100.0%; Pred. No. 1.9e+04;
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/clone_lib="Sanger Institute Gene Trap Library pGT0lxfT2"
/note="Vector: pGT0lxfT2"
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                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Sanger Intitute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2013)
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Bmail: info.genetrap@asanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
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Contact: Walbot V
Department of Biological Sciences
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Plate: 1006100 row: 31
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/mol type="mmn" paptrine
/db xref="taxon.9606"
/clone_lib="Compugen_targeted_mRNA_sequencing"
/note="These sequences resulted from single pass
sequencing project. PKR products from Compugen targeted mRNA
sequencing project. PKR primers and nested primers were
designed to join two neighboring expressed sequence
contigs based on Compugen LEADS expressed sequence cluster
and assembly platform. Reverse transcriptase PKR and
nested PCR reactions were performed by Protedyne Inc.
(Windsor, CT 06095, USA) on normal human heart, brain,
described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on many availability can be found at: 'trip'/www.mpiz-koeln.mpine availability can be found at: Location/Qualifiers
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                                                                                                                                                                                                                                                           /clone="GK-303A11-015563"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
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Fax: 609-655-5114
Email: han@cgen.com.
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ઠ 셤 The same

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gql 4732114)gbl AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
Invitrogen (Carlsbad, California 92008). PCR products were sequenced by Qiagen (Valencia, CA 91355)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZEJOYS6 83 bp DNA . linear GSS 20-FEB-2001 2M0110P22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0110P22 F, genomic survey sequence. AZEJO956
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
1 (bases 1 to 83)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clome lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                  Length 81;
                                                                                                                           41.4%; Score 12; DB 5; Le
100.0%; Pred. No. 1.9e+04;
ive 0; Mismatches 0;
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Pax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: P column: 22
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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Location/Qualifiers
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Mus musculus
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                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 12, Conservative
                                                                                                                                                                                                                                                                  12 TACCATAGAGCC 23
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6, 2006, 00:16:52

Search completed: March Job time : 2990.5 secs

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Direct Submission

Submitteed (13-0CT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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GSS, left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="424808"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                                                                                       DB 9; Length 83;
1.9e+04;
                                                                                                                                                                                              0; Indels

    .83
    note="T-DNA flanking sequence"

                                                                                                                                       Query Match 41.4%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 1.9 Matches 12; Conservative 0; Mismatches
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Balzergue, S.
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VERSION
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AUTHORS
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